

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 10:26:31 ; Search time 1926 Seconds
(without alignments)
9044.356 Million cell updates/sec

Title: US-09-898-556A-3
Perfect score: 2772
Sequence: 1 cagcgcggttaagctgtgtg.....tttaccacatctaccct 2772

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7090273 seqs, 3142032823 residues

Total number of hits satisfying chosen parameters: 7894758

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCN_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	1.2	51	5	US-09-749-280B-127
2	33	1.2	41	11	US-60-449-155-509
3	31.6	1.1	51	5	US-09-749-280B-128
4	27.8	1.0	55	6	US-09-912-293-242606
5	27	1.0	60	1	PCT-US03-02358-36
6	27	1.0	60	5	US-09-911-261B-36
7	27	1.0	60	6	US-09-911-261A-36
8	26.8	1.0	51	5	US-09-749-280B-5554
9	26.8	1.0	51	5	US-09-749-280B-6407
10	26.6	1.0	56	1	PCT-US03-02358-49
11	26.6	1.0	56	5	US-09-911-261B-49
12	26.6	1.0	56	5	US-09-911-261A-49
13	25.8	0.9	60	1	PCT-US03-02358-45
14	25.8	0.9	60	5	US-09-911-261B-45
15	25.8	0.9	60	6	US-09-911-261A-45
16	25.6	0.9	56	1	PCT-US03-02358-40
17	25.6	0.9	56	5	US-09-911-261B-40
18	25.6	0.9	56	5	US-09-911-261A-40
19	25.2	0.9	50	9	US-10-325-899-2511
20	25.2	0.9	50	9	US-10-325-899-3660
21	25.2	0.9	51	5	US-09-749-280B-519
22	24.6	0.9	55	1	PCT-US03-02358-50

23	24.6	0.9	55	5	US-09-911-261B-50	Sequence 50, App1
24	24.6	0.9	55	6	US-09-911-261A-50	Sequence 50, App1
25	24.4	0.9	51	5	US-09-749-280B-5867	Sequence 5867, Ap
26	24.4	0.9	51	5	US-09-749-280B-6408	Sequence 6408, Ap
27	23.8	0.9	55	1	PCT-US03-02358-41	Sequence 41, App1
28	23.8	0.9	55	5	US-09-911-261B-41	Sequence 41, App1
29	23.8	0.9	55	6	US-09-911-261A-41	Sequence 41, App1
30	23.8	0.9	58	6	US-10-310-156A-470	Sequence 470, App
31	23.8	0.9	58	9	US-10-310-156B-470	Sequence 470, App
32	23	0.8	59	6	US-09-912-293-732	Sequence 732, App
33	22.4	0.8	41	11	US-60-449-155-516	Sequence 516, App
34	22.4	0.8	60	1	PCT-US03-02358-39	Sequence 39, App1
35	22.4	0.8	60	1	PCT-US03-02358-48	Sequence 48, App1
36	22.4	0.8	60	5	US-09-911-261B-39	Sequence 39, App1
37	22.4	0.8	60	5	US-09-911-261B-48	Sequence 48, App1
38	22.4	0.8	60	6	US-09-911-261A-39	Sequence 39, App1
39	22.4	0.8	60	6	US-09-911-261A-48	Sequence 48, App1
40	22.2	0.8	51	5	US-09-749-280B-6410	Sequence 6410, Ap
41	21.8	0.8	25	11	US-60-427-808-134357	Sequence 134357,
42	21.8	0.8	25	11	US-60-427-836-480873	Sequence 480873,
43	21.8	0.8	41	11	US-60-449-155-517	Sequence 517, App
44	21.8	0.8	50	1	PCT-US03-11497-11	Sequence 11, App1
45	21.8	0.8	60	9	US-10-257-848-81	Sequence 81, App1
46	21.6	0.8	50	9	US-10-325-899-4332	Sequence 4332, Ap
47	21.4	0.8	50	5	US-09-749-280B-5462	Sequence 5462, Ap
48	21.4	0.8	50	9	US-10-325-899-4844	Sequence 4844, Ap
49	21.2	0.8	50	5	US-09-749-280B-1151	Sequence 1151, Ap
50	21.2	0.8	50	8	US-10-089-560-10	Sequence 10, App1
51	21.2	0.8	50	9	US-10-325-899-4458	Sequence 4458, Ap
52	21	0.8	45	1	PCT-US03-02358-56	Sequence 56, App1
53	21	0.8	45	5	US-09-911-261B-56	Sequence 56, App1
54	21	0.8	45	6	US-09-911-261A-56	Sequence 56, App1
55	21	0.8	48	8	US-10-402-954-19	Sequence 19, App1
56	21	0.8	50	5	US-09-749-280B-5461	Sequence 5461, Ap
57	21	0.8	52	4	US-08-908-156A-72	Sequence 72, App1
58	21	0.8	53	4	US-08-906-156B-72	Sequence 72, App1
59	21	0.8	53	6	US-09-912-293-243046	Sequence 243046,
60	21	0.8	59	8	US-09-912-293-2236	Sequence 2236, App
61	20.8	0.8	25	11	US-60-427-808-134407	Sequence 134407,
62	20.8	0.8	50	9	US-10-325-899-1400	Sequence 1400, Ap
63	20.8	0.8	51	5	US-09-749-280B-522	Sequence 522, Ap
64	20.8	0.8	53	6	US-09-912-293-62705	Sequence 62705, A
65	20.8	0.8	56	6	US-09-912-293-153278	Sequence 153278,
66	20.8	0.8	56	6	US-09-912-293-243169	Sequence 243169,
67	20.6	0.7	27	1	PCT-US03-05186-47	Sequence 47, App1
68	20.6	0.7	51	5	US-09-749-280B-1308	Sequence 1308, Ap
69	20.6	0.7	51	5	US-09-749-280B-2579	Sequence 2579, Ap
70	20.6	0.7	52	8	US-10-409-627-244	Sequence 244, App
71	20.6	0.7	56	6	US-09-912-293-89289	Sequence 89289, A
72	20.6	0.7	60	8	US-10-193-926A-16	Sequence 16, App1
73	20.6	0.7	60	9	US-10-193-747-25	Sequence 25, App1
74	20.6	0.7	60	9	US-10-193-747-26	Sequence 26, App1
75	20.6	0.7	60	9	US-10-316-954-1179	Sequence 1179, Ap
76	20.6	0.7	60	9	US-10-316-954-2828	Sequence 2828, Ap
77	20.6	0.7	60	9	US-10-349-781-19132	Sequence 19132, A
78	20.4	0.7	49	8	US-10-287-787-17660	Sequence 7660, Ap
79	20.4	0.7	50	5	US-09-749-280B-1163	Sequence 3163, Ap
80	20.4	0.7	50	8	US-10-287-787-7659	Sequence 7659, Ap
81	20.4	0.7	50	9	US-10-325-899-201	Sequence 201, App
82	20.4	0.7	51	1	PCT-US03-00669A-13	Sequence 13, App1
83	20.4	0.7	51	5	US-09-749-280B-944	Sequence 944, App
84	20.4	0.7	52	7	US-09-837-604A-19233	Sequence 49333, A
85	20.2	0.7	25	11	US-60-427-808-134358	Sequence 134358,
86	20.2	0.7	25	11	US-60-427-808-453684	Sequence 453684,
87	20.2	0.7	25	11	US-60-427-808-453687	Sequence 453687,
88	20.2	0.7	25	11	US-60-427-808-872650	Sequence 872650,
89	20.2	0.7	25	11	US-60-427-836-289684	Sequence 289684,
90	20.2	0.7	25	11	US-60-427-836-480872	Sequence 480872,
91	20.2	0.7	25	11	US-60-427-836-5000278	Sequence 5000278,
92	20.2	0.7	45	9	US-10-321-853-250	Sequence 250, App
93	20.2	0.7	47	9	US-10-349-143-201	Sequence 201, App
94	20.2	0.7	50	5	US-09-749-280B-2146	Sequence 2146, Ap
95	20.2	0.7	50	9	US-10-325-899-1747	Sequence 1747, Ap

96	20.2	0.7	50	9	US-10-325-899-2954	Sequence 2954, Ap	C 169	19.4	0.7	56	6	US-09-912-293-189098	Sequence 189098,
C 97	20.2	0.7	50	9	US-10-325-899-6159	Sequence 6159, Ap	C 170	19.4	0.7	56	9	US-10-136-159A-106	Sequence 106, App
C 98	20.2	0.7	50	9	US-10-325-899-6222	Sequence 6222, Ap	C 171	19.4	0.7	57	1	PCT-US02-40891-975	Sequence 975, App
C 99	20.2	0.7	50	9	US-10-325-899-6355	Sequence 6355, Ap	C 172	19.4	0.7	57	1	PCT-US02-40891-977	Sequence 977, App
100	20.2	0.7	50	9	US-10-325-899-7334	Sequence 7334, Ap	C 173	19.4	0.7	57	1	PCT-US02-40892-307	Sequence 307, App
C 101	20.2	0.7	50	9	US-10-325-899-7546	Sequence 7546, Ap	C 174	19.4	0.7	57	1	PCT-US02-40892-309	Sequence 309, App
C 102	20.2	0.7	51	5	US-09-749-2808-1282	Sequence 1282, Ap	C 175	19.4	0.7	57	1	PCT-US02-40892A-307	Sequence 307, App
C 103	20.2	0.7	51	5	US-09-749-2808-3411	Sequence 3411, Ap	C 176	19.4	0.7	57	1	PCT-US02-40892A-309	Sequence 309, App
C 104	20.2	0.7	57	9	US-10-321-853-297	Sequence 297, App	C 177	19.4	0.7	57	8	US-10-287-787-3416	Sequence 3416, App
C 105	20.2	0.7	60	8	US-10-384-850-16	Sequence 16, App1	C 178	19.4	0.7	60	1	PCT-US03-04142-56	Sequence 3416, App
106	20.2	0.7	60	11	US-60-288-292-4771	Sequence 4771, Ap	C 179	19.4	0.7	60	6	US-09-534-850-16126	Sequence 58, App1
C 107	20	0.7	47	9	US-10-316-957-279	Sequence 279, App	C 180	19.2	0.7	25	6	US-09-866-108A-14627	Sequence 16126, A
C 108	20	0.7	47	9	US-10-316-957-280	Sequence 280, App	C 181	19.2	0.7	25	6	US-09-866-108A-14628	Sequence 14628, A
C 109	20	0.7	47	9	US-10-316-957-281	Sequence 281, App	C 182	19.2	0.7	25	11	US-60-427-808-72571	Sequence 14628, A
C 110	20	0.7	51	5	US-09-749-2808-535	Sequence 535, App	C 183	19.2	0.7	25	11	US-60-427-808-72571	Sequence 72571, A
C 111	19.8	0.7	25	6	US-09-660-222-139796	Sequence 139796,	C 184	19.2	0.7	25	11	US-60-427-808-134409	Sequence 134409,
C 112	19.8	0.7	25	6	US-10-355-577-911174	Sequence 911174,	C 185	19.2	0.7	25	11	US-60-427-808-336016	Sequence 336016,
C 113	19.8	0.7	25	11	US-60-427-808-8553	Sequence 8553, Ap	C 186	19.2	0.7	25	11	US-60-427-808-336017	Sequence 336017,
C 114	19.8	0.7	25	11	US-60-427-808-142838	Sequence 142838,	C 187	19.2	0.7	25	11	US-60-427-808-440447	Sequence 440447,
C 115	19.8	0.7	25	11	US-60-427-808-452331	Sequence 452331,	C 188	19.2	0.7	25	11	US-60-427-808-601832	Sequence 601832,
C 116	19.8	0.7	25	11	US-60-427-808-432333	Sequence 432333,	C 189	19.2	0.7	25	11	US-60-427-808-766984	Sequence 766984,
C 117	19.8	0.7	25	11	US-60-427-808-820370	Sequence 820370,	C 190	19.2	0.7	25	11	US-60-427-808-770573	Sequence 770573,
C 118	19.8	0.7	25	11	US-60-427-836-118717	Sequence 118717,	C 191	19.2	0.7	25	11	US-60-427-808-861714	Sequence 861714,
C 119	19.8	0.7	40	8	US-10-287-787-21150	Sequence 21150, A	C 192	19.2	0.7	25	11	US-60-427-808-903557	Sequence 903557,
C 120	19.8	0.7	47	9	US-10-349-143-1468	Sequence 1468, A	C 193	19.2	0.7	25	11	US-60-427-808-903557	Sequence 903557,
C 121	19.8	0.7	47	9	US-10-333-429-165	Sequence 165, App	C 194	19.2	0.7	41	11	US-60-449-155-512	Sequence 276629,
C 122	19.8	0.7	50	5	US-09-749-2808-4178	Sequence 4178, App	C 195	19.2	0.7	41	11	US-60-449-155-518	Sequence 518, App
C 123	19.8	0.7	50	5	US-10-325-899-2798	Sequence 2798, Ap	C 196	19.2	0.7	47	9	US-10-349-143-802	Sequence 802, App
C 124	19.8	0.7	50	9	US-10-325-899-4602	Sequence 4602, Ap	C 197	19.2	0.7	47	9	US-10-349-143-186	Sequence 1486, Ap
C 125	19.8	0.7	50	9	US-10-325-899-7294	Sequence 7294, Ap	C 198	19.2	0.7	47	9	US-10-349-143-236	Sequence 2536, Ap
C 126	19.8	0.7	51	1	PCT-US03-00669A-17	Sequence 17, App1	C 199	19.2	0.7	47	9	US-10-349-143-2859	Sequence 2859, Ap
C 127	19.8	0.7	51	5	US-09-749-2808-257	Sequence 257, App	C 200	19.2	0.7	47	9	US-10-349-143-3534	Sequence 3534, Ap
C 128	19.8	0.7	51	5	US-09-749-2808-6113	Sequence 6113, Ap	C 201	19.2	0.7	49	11	US-10-349-143-3766	Sequence 3766, Ap
C 129	19.8	0.7	57	6	US-09-500-700-47	Sequence 47, App1	C 202	19.2	0.7	50	5	US-60-288-282-18118	Sequence 38178, A
C 130	19.8	0.7	57	11	US-60-449-055-23	Sequence 23, App1	C 203	19.2	0.7	50	5	US-09-749-2808-1474	Sequence 1474, Ap
C 131	19.8	0.7	58	5	US-09-513-999C-18026	Sequence 18026, A	C 204	19.2	0.7	50	5	US-09-749-2808-7215	Sequence 7215, Ap
C 132	19.8	0.7	58	6	US-09-513-999C-18026	Sequence 18026, A	C 205	19.2	0.7	50	9	US-10-325-899-853	Sequence 853, App
C 133	19.8	0.7	58	8	US-10-287-787-10059	Sequence 10059, A	C 206	19.2	0.7	50	9	US-10-325-899-2847	Sequence 2847, Ap
C 134	19.8	0.7	58	8	US-10-287-787-10201	Sequence 10201, A	C 207	19.2	0.7	50	9	US-10-325-899-3021	Sequence 3021, Ap
C 135	19.8	0.7	58	8	US-10-287-787-14769	Sequence 14769, A	C 208	19.2	0.7	51	5	US-09-749-2808-3794	Sequence 3794, Ap
C 136	19.8	0.7	60	9	US-10-329-624-1661	Sequence 1661, Ap	C 209	19.2	0.7	51	5	US-09-749-2808-682	Sequence 682, Ap
C 137	19.6	0.7	47	9	US-10-349-143-1331	Sequence 1231, Ap	C 210	19.2	0.7	51	6	US-09-749-2808-7734	Sequence 7734, Ap
C 138	19.6	0.7	47	9	US-10-349-143-1331	Sequence 1231, Ap	C 211	19.2	0.7	51	6	US-09-922-222A-111	Sequence 2724, Ap
C 139	19.6	0.7	48	6	US-09-863-041-3163	Sequence 3797, Ap	C 212	19.2	0.7	57	6	US-09-912-293-199375	Sequence 111, App
C 140	19.6	0.7	48	7	US-10-325-899-3398	Sequence 3163, Ap	C 213	19.2	0.7	57	6	US-10-198-069-30	Sequence 199375,
C 141	19.6	0.7	50	9	US-10-325-899-3398	Sequence 3163, Ap	C 214	19.2	0.7	58	1	PCT-US03-14114-2821	Sequence 30, App1
C 142	19.6	0.7	50	9	US-10-325-899-3398	Sequence 3163, Ap	C 215	19.2	0.7	58	1	PCT-US03-14114-2822	Sequence 2821, Ap
C 143	19.6	0.7	51	5	US-09-749-2808-3132	Sequence 3947, Ap	C 216	19.2	0.7	58	1	PCT-US03-14114-2823	Sequence 2823, Ap
C 144	19.6	0.7	51	5	US-09-749-2808-5866	Sequence 5866, Ap	C 217	19.2	0.7	59	6	US-09-677-653A-53	Sequence 2823, Ap
C 145	19.6	0.7	51	5	US-09-749-2808-6197	Sequence 6197, Ap	C 218	19.2	0.7	59	6	US-09-677-653A-53	Sequence 53, App1
C 146	19.6	0.7	51	5	US-09-749-2808-6197	Sequence 6197, Ap	C 219	19.2	0.7	59	6	US-09-912-293-42307	Sequence 53, App1
C 147	19.6	0.7	58	9	US-10-102-143-30	Sequence 6359, Ap	C 220	19.2	0.7	60	11	US-10-349-781-50706	Sequence 42307, A
C 148	19.4	0.7	43	6	US-09-136-159-99	Sequence 30, App1	C 221	19	0.7	60	11	US-60-422-176-685	Sequence 50706, A
C 149	19.4	0.7	43	6	US-09-136-159-99	Sequence 99, App1	C 222	19	0.7	30	6	US-09-980-559-31	Sequence 685, App
C 150	19.4	0.7	43	6	US-09-136-159A-99	Sequence 99, App1	C 223	19	0.7	30	6	US-09-785-632B-80	Sequence 31, App1
C 151	19.4	0.7	45	1	PCT-US02-38450-163	Sequence 163, App	C 224	19	0.7	47	9	US-10-257-549-93	Sequence 80, App1
C 152	19.4	0.7	45	1	PCT-US02-38450-163	Sequence 163, App	C 225	19	0.7	47	9	US-10-349-143-1679	Sequence 53, App1
C 153	19.4	0.7	45	5	US-09-911-261B-54	Sequence 54, App1	C 226	19	0.7	48	1	PCT-US03-02358-43	Sequence 1679, Ap
C 154	19.4	0.7	45	5	US-09-911-261B-54	Sequence 54, App1	C 227	19	0.7	48	1	PCT-US03-02358-43	Sequence 43, App1
C 155	19.4	0.7	47	9	US-10-349-143-1304	Sequence 54, App1	C 228	19	0.7	48	1	PCT-US03-02358-43	Sequence 43, App1
C 156	19.4	0.7	48	8	US-10-367-892-6822	Sequence 1304, Ap	C 229	19	0.7	48	6	US-09-911-261A-43	Sequence 43, App1
C 157	19.4	0.7	49	11	US-60-288-292-10249	Sequence 6822, Ap	C 230	19	0.7	50	1	PCT-US03-13015-596	Sequence 56, App
C 158	19.4	0.7	50	9	US-09-749-2808-1274	Sequence 10249, A	C 231	19	0.7	50	5	US-09-749-2808-7164	Sequence 7164, Ap
C 159	19.4	0.7	50	9	US-10-325-899-2323	Sequence 1274, Ap	C 232	19	0.7	50	6	US-09-906-777B-57	Sequence 762, Ap
C 160	19.4	0.7	50	9	US-10-325-899-2323	Sequence 2323, Ap	C 233	19	0.7	50	6	US-09-904-011C-57	Sequence 57, App1
C 161	19.4	0.7	50	9	US-10-325-899-3870	Sequence 3870, Ap	C 234	19	0.7	50	6	US-09-665-350B-57	Sequence 57, App1
C 162	19.4	0.7	51	5	US-09-749-2808-2318	Sequence 4042, Ap	C 235	19	0.7	50	8	US-10-426-504-57	Sequence 57, App1
C 163	19.4	0.7	51	5	US-09-749-2808-2318	Sequence 2318, Ap	C 236	19	0.7	50	8	US-10-426-504-57	Sequence 57, App1
C 164	19.4	0.7	54	6	US-09-912-293-219013	Sequence 3575, Ap	C 237	19	0.7	50	8	US-10-427-239-57	Sequence 57, App1
C 165	19.4	0.7	54	8	US-10-287-919-1217	Sequence 219013,	C 238	19	0.7	50	8	US-10-425-447-57	Sequence 57, App1
C 166	19.4	0.7	54	8	US-10-287-919-1217	Sequence 1217, Ap	C 239	19	0.7	50	9	US-10-299-937-57	Sequence 57, App1
C 167	19.4	0.7	56	6	US-09-136-159-106	Sequence 106, App	C 240	19	0.7	50	9	US-10-299-976-57	Sequence 57, App1
C 168	19.4	0.7	56	6	US-09-136-159A-106	Sequence 106, App	C 241	19	0.7	50	9	US-10-325-899-3046	Sequence 3046, Ap

C 242	19	0.7	50	9	US-10-325-899-3080	Sequence 3080, Ap	315	18.6	0.7	25	11	US-60-427-808-470381	Sequence 470381,
C 243	19	0.7	50	9	US-10-325-899-4654	Sequence 4654, Ap	316	18.6	0.7	25	11	US-60-427-808-596271	Sequence 596271,
C 244	19	0.7	50	9	US-10-325-899-6375	Sequence 6375, Ap	317	18.6	0.7	25	11	US-60-427-808-780060	Sequence 780060,
C 245	19	0.7	51	5	US-09-749-2808-823	Sequence 823, App	318	18.6	0.7	25	11	US-60-427-808-841637	Sequence 841637,
C 246	19	0.7	51	5	US-09-749-2808-1311	Sequence 1311, Ap	319	18.6	0.7	25	11	US-60-427-808-872649	Sequence 872649,
C 247	19	0.7	51	5	US-09-749-2808-1800	Sequence 1800, Ap	320	18.6	0.7	25	11	US-60-427-808-921866	Sequence 921866,
C 248	19	0.7	51	5	US-09-749-2808-2443	Sequence 2443, Ap	321	18.6	0.7	25	11	US-60-427-808-972582	Sequence 972582,
C 249	19	0.7	51	5	US-09-749-2808-6145	Sequence 6145, Ap	322	18.6	0.7	25	11	US-60-427-836-112977	Sequence 112977,
C 250	19	0.7	53	6	US-09-912-293-37171	Sequence 37171, A	323	18.6	0.7	25	11	US-60-427-836-224332	Sequence 224332,
C 251	19	0.7	55	6	PCT-US02-41414-648	Sequence 648, App	324	18.6	0.7	25	11	US-60-427-836-224332	Sequence 224332,
C 252	19	0.7	55	5	US-09-513-999C-33160	Sequence 33160, A	325	18.6	0.7	25	11	US-60-427-836-255224	Sequence 255224,
C 253	19	0.7	55	6	US-09-513-999C-33160	Sequence 33160, A	326	18.6	0.7	25	11	US-60-427-836-269085	Sequence 269085,
C 254	19	0.7	57	6	US-09-513-999C-33160	Sequence 33160, A	327	18.6	0.7	25	11	US-60-427-836-289683	Sequence 289683,
C 255	19	0.7	57	11	US-09-674-109B-14	Sequence 32220, A	328	18.6	0.7	25	11	US-60-427-836-335122	Sequence 335122,
C 256	19	0.7	60	6	PCT-US03-04142-33	Sequence 33, App1	329	18.6	0.7	25	11	US-60-427-836-436989	Sequence 436989,
C 257	19	0.7	60	6	US-09-688-6712A-98	Sequence 98, App1	330	18.6	0.7	25	11	US-60-427-836-500279	Sequence 500279,
C 258	19	0.7	60	6	US-09-539-806B-44516	Sequence 44516, A	331	18.6	0.7	25	11	US-60-427-836-594118	Sequence 594118,
C 259	19	0.7	60	7	US-10-304-133A-1693	Sequence 1693, Ap	332	18.6	0.7	25	11	US-60-427-836-594119	Sequence 594119,
C 260	19	0.7	60	8	US-10-355-577-706026	Sequence 706026, A	333	18.6	0.7	25	11	US-60-427-836-604205	Sequence 604205,
C 261	18.8	0.7	25	9	US-10-349-143-250	Sequence 115595, A	334	18.6	0.7	25	11	PCT-US02-41033-18	Sequence 636338,
C 262	18.8	0.7	25	11	US-60-417-190-115595	Sequence 115595, A	335	18.6	0.7	45	1	US-10-349-143-416	Sequence 416, App1
C 263	18.8	0.7	25	11	US-60-417-190-115595	Sequence 115595, A	336	18.6	0.7	47	9	US-10-349-143-2717	Sequence 2717, App
C 264	18.8	0.7	25	11	US-60-427-808-166136	Sequence 166136, A	337	18.6	0.7	48	8	US-10-369-493-29517	Sequence 29517, A
C 265	18.8	0.7	25	11	US-60-427-808-349668	Sequence 349668, A	338	18.6	0.7	49	9	US-10-316-957-166	Sequence 166, App
C 266	18.8	0.7	25	11	US-60-427-808-738154	Sequence 738154, A	339	18.6	0.7	49	9	US-10-316-957-167	Sequence 167, App
C 267	18.8	0.7	25	11	US-60-427-836-346667	Sequence 346667, A	340	18.6	0.7	50	1	PCT-US03-13015-646	Sequence 646, App
C 268	18.8	0.7	25	11	US-60-427-836-500855	Sequence 500855, A	341	18.6	0.7	50	1	PCT-US03-14114-2843	Sequence 2843, App
C 269	18.8	0.7	25	11	US-60-427-836-526622	Sequence 526622, A	342	18.6	0.7	50	1	PCT-US03-14114-2843	Sequence 2843, App
C 270	18.8	0.7	25	11	US-60-427-836-567430	Sequence 567430, A	343	18.6	0.7	50	1	PCT-US03-14114-2843	Sequence 2843, App
C 271	18.8	0.7	25	11	US-60-427-836-625309	Sequence 625309, A	344	18.6	0.7	50	1	US-09-749-2808-6876	Sequence 6876, App
C 272	18.8	0.7	47	9	US-10-298-214-10	Sequence 10, App1	345	18.6	0.7	50	5	US-09-749-2808-7367	Sequence 7367, App
C 273	18.8	0.7	47	9	US-10-349-143-250	Sequence 250, App	346	18.6	0.7	50	5	US-10-325-899-960	Sequence 960, App
C 274	18.8	0.7	47	9	US-10-349-143-350	Sequence 350, App	347	18.6	0.7	50	9	US-10-325-899-3079	Sequence 3079, App
C 275	18.8	0.7	49	8	US-10-385-450-6	Sequence 6, App1	348	18.6	0.7	50	9	US-10-325-899-3358	Sequence 3358, App
C 276	18.8	0.7	50	1	PCT-US03-02612-1150	Sequence 160, App	349	18.6	0.7	50	9	US-10-325-899-4532	Sequence 4532, App
C 277	18.8	0.7	50	5	US-09-749-2808-1160	Sequence 1160, App	350	18.6	0.7	50	9	US-10-325-899-4538	Sequence 4538, App
C 278	18.8	0.7	50	5	US-09-749-2808-3916	Sequence 3916, App	351	18.6	0.7	50	9	US-10-325-899-5052	Sequence 5052, App
C 279	18.8	0.7	50	9	US-10-325-899-457	Sequence 457, App	352	18.6	0.7	50	9	US-10-325-899-6613	Sequence 6613, App
C 280	18.8	0.7	50	9	US-10-325-899-1759	Sequence 1759, App	353	18.6	0.7	50	9	US-10-325-899-7003	Sequence 7003, App
C 281	18.8	0.7	50	9	US-10-325-899-2871	Sequence 2871, App	354	18.6	0.7	50	9	US-10-325-899-7577	Sequence 7577, App
C 282	18.8	0.7	50	9	US-10-325-899-3712	Sequence 3712, App	355	18.6	0.7	50	9	US-10-325-899-7597	Sequence 7597, App
C 283	18.8	0.7	50	9	US-10-325-899-3898	Sequence 3898, App	356	18.6	0.7	51	5	US-09-749-2808-846	Sequence 846, App
C 284	18.8	0.7	51	5	US-10-325-899-3684	Sequence 3684, App	357	18.6	0.7	51	5	US-09-749-2808-6283	Sequence 6283, App
C 285	18.8	0.7	51	5	US-09-749-2808-1130	Sequence 1130, App	358	18.6	0.7	54	6	US-09-912-293-166212	Sequence 166212, A
C 286	18.8	0.7	51	8	US-10-272-358-10	Sequence 10, App1	359	18.6	0.7	55	1	PCT-US01-43588-72	Sequence 72, App1
C 287	18.8	0.7	51	8	US-10-407-461-45	Sequence 45, App1	360	18.6	0.7	55	1	PCT-US01-43588-72	Sequence 72, App1
C 288	18.8	0.7	53	6	US-09-912-293-175133	Sequence 175133, A	361	18.6	0.7	56	5	US-09-513-999C-27257	Sequence 27257, A
C 289	18.8	0.7	56	9	US-10-019-258-23	Sequence 23, App1	362	18.6	0.7	56	6	US-09-513-999C-27257	Sequence 27257, A
C 290	18.8	0.7	58	5	US-09-513-999C-15215	Sequence 15215, A	363	18.6	0.7	56	6	US-09-912-293-138761	Sequence 138761, A
C 291	18.8	0.7	58	6	US-09-513-999C-15215	Sequence 15215, A	364	18.6	0.7	56	6	US-09-912-293-211959	Sequence 211959, A
C 292	18.8	0.7	59	6	US-09-708-506A-12	Sequence 12, App1	365	18.6	0.7	56	9	US-10-325-899-5140	Sequence 5140, App
C 293	18.8	0.7	59	8	US-10-287-820-1160	Sequence 1160, App	366	18.6	0.7	57	8	US-10-294-037A-1477	Sequence 1477, App
C 294	18.8	0.7	60	8	US-10-372-730-17	Sequence 17, App1	367	18.6	0.7	57	9	US-10-316-957-2788	Sequence 2788, App
C 295	18.6	0.7	25	6	US-09-866-108A-14626	Sequence 14626, App	368	18.6	0.7	57	9	US-10-316-957-2789	Sequence 2789, App
C 296	18.6	0.7	25	9	US-10-098-263B-59357	Sequence 59357, A	369	18.6	0.7	57	9	US-10-316-957-2790	Sequence 2790, App
C 297	18.6	0.7	25	9	US-10-355-577-151132	Sequence 151132, A	370	18.6	0.7	58	6	US-09-912-293-18132	Sequence 18132, A
C 298	18.6	0.7	25	9	US-10-355-577-583946	Sequence 583946, A	371	18.6	0.7	60	4	PCT-US03-04213-74	Sequence 24, App1
C 299	18.6	0.7	25	9	US-10-355-577-669381	Sequence 669381, A	372	18.6	0.7	60	4	US-08-457-855E-22	Sequence 22, App1
C 300	18.6	0.7	25	9	US-10-355-577-956983	Sequence 956983, A	373	18.6	0.7	60	5	US-09-931-732C-51	Sequence 51, App1
C 301	18.6	0.7	25	11	US-60-417-190-115601	Sequence 115601, A	374	18.6	0.7	60	9	US-10-365-095-24	Sequence 24, App1
C 302	18.6	0.7	25	11	US-60-427-808-93243	Sequence 93243, A	375	18.6	0.7	25	9	US-10-355-577-202504	Sequence 202504, A
C 303	18.6	0.7	25	11	US-60-427-808-117447	Sequence 117447, A	376	18.4	0.7	25	11	US-60-427-808-136653	Sequence 136653, A
C 304	18.6	0.7	25	11	US-60-427-808-126633	Sequence 126633, A	377	18.4	0.7	25	11	US-60-427-808-197879	Sequence 197879, A
C 305	18.6	0.7	25	11	US-60-427-808-168700	Sequence 168700, A	378	18.4	0.7	25	11	US-60-427-808-237128	Sequence 237128, A
C 306	18.6	0.7	25	11	US-60-427-808-205145	Sequence 205145, A	379	18.4	0.7	25	11	US-60-427-808-542617	Sequence 542617, A
C 307	18.6	0.7	25	11	US-60-427-808-229054	Sequence 229054, A	380	18.4	0.7	25	11	US-60-427-836-137687	Sequence 137687, A
C 308	18.6	0.7	25	11	US-60-427-808-290348	Sequence 290348, A	381	18.4	0.7	31	9	US-10-274-616-33	Sequence 33, App1
C 309	18.6	0.7	25	11	US-60-427-808-401173	Sequence 401173, A	382	18.4	0.7	33	9	US-10-316-954-2218	Sequence 2218, App
C 310	18.6	0.7	25	11	US-60-427-808-401174	Sequence 401174, A	383	18.4	0.7	33	9	US-10-316-954-2450	Sequence 2450, App
C 311	18.6	0.7	25	11	US-60-427-808-419733	Sequence 419733, A	384	18.4	0.7	36	8	US-10-287-820-1235	Sequence 1235, App
C 312	18.6	0.7	25	11	US-60-427-808-445052	Sequence 445052, A	385	18.4	0.7	39	9	US-10-207-745A-7	Sequence 7, App1
C 313	18.6	0.7	25	11	US-60-427-808-445053	Sequence 445053, A	386	18.4	0.7	40	1	PCT-US03-04946-6	Sequence 6, App1
C 314	18.6	0.7	25	11	US-60-427-808-456425	Sequence 456425, A	387	18.4	0.7	40	8	US-10-370-052-6	Sequence 6, App1

C 388	18.4	0.7	44	9	US-10-367-169-99	Sequence 99, App1
C 389	18.4	0.7	47	9	US-10-294-934-648	Sequence 648, App
C 390	18.4	0.7	47	9	US-10-349-143-1645	Sequence 1645, App
C 391	18.4	0.7	47	9	US-10-349-143-3265	Sequence 3265, App
C 392	18.4	0.7	48	9	US-10-230-006-2531	Sequence 2531, App
C 393	18.4	0.7	50	1	PCT-US03-13015-846	Sequence 846, App
C 394	18.4	0.7	50	5	US-09-749-2808-4273	Sequence 4273, App
C 395	18.4	0.7	50	5	US-09-749-2808-6790	Sequence 6790, App
C 396	18.4	0.7	50	5	US-09-749-2808-7682	Sequence 7682, App
C 397	18.4	0.7	50	5	US-09-749-2808-7843	Sequence 7843, App
C 398	18.4	0.7	50	9	US-10-325-899-1033	Sequence 1033, App
C 399	18.4	0.7	50	9	US-10-325-899-3408	Sequence 3408, App
C 400	18.4	0.7	50	9	US-10-325-899-4262	Sequence 4262, App
C 401	18.4	0.7	50	9	US-10-325-899-5027	Sequence 5027, App
C 402	18.4	0.7	50	9	US-10-325-899-5530	Sequence 5530, App
C 403	18.4	0.7	50	9	US-10-325-899-7586	Sequence 7586, App
C 404	18.4	0.7	51	1	PCT-US02-40891-1971	Sequence 1971, App
C 405	18.4	0.7	51	1	PCT-US02-40892-746	Sequence 746, App
C 406	18.4	0.7	51	5	US-09-749-2808-746	Sequence 746, App
C 407	18.4	0.7	51	5	US-09-749-2808-3313	Sequence 3313, App
C 408	18.4	0.7	51	5	US-09-749-2808-4324	Sequence 4324, App
C 409	18.4	0.7	51	5	US-09-749-2808-4325	Sequence 4325, App
C 410	18.4	0.7	51	5	US-09-749-2808-6362	Sequence 6362, App
C 411	18.4	0.7	53	8	US-10-294-041A-2131	Sequence 2131, App
C 412	18.4	0.7	53	9	US-10-316-957-1065	Sequence 1065, App
C 413	18.4	0.7	53	9	US-10-316-957-1066	Sequence 1066, App
C 414	18.4	0.7	53	9	US-10-316-957-1067	Sequence 1067, App
C 415	18.4	0.7	53	9	US-10-316-957-1068	Sequence 1068, App
C 416	18.4	0.7	53	9	US-10-321-853-978	Sequence 978, App
C 417	18.4	0.7	53	9	US-10-321-853-979	Sequence 979, App
C 418	18.4	0.7	53	9	US-10-321-853-980	Sequence 980, App
C 419	18.4	0.7	53	9	US-10-321-853-981	Sequence 981, App
C 420	18.4	0.7	54	1	PCT-US03-0069A-15	Sequence 981, App
C 421	18.4	0.7	54	6	US-09-912-293-93470	Sequence 93470, App
C 422	18.4	0.7	54	9	US-10-316-957-2112	Sequence 2112, App
C 423	18.4	0.7	54	9	US-10-316-957-2113	Sequence 2113, App
C 424	18.4	0.7	54	9	US-10-316-957-2114	Sequence 2114, App
C 425	18.4	0.7	54	9	US-10-316-957-2115	Sequence 2115, App
C 426	18.4	0.7	56	6	US-09-912-293-15565	Sequence 15565, App
C 427	18.4	0.7	57	6	US-10-321-853-1986	Sequence 1986, App
C 428	18.4	0.7	58	6	US-09-912-293-73123	Sequence 73123, App
C 429	18.4	0.7	58	10	US-09-912-293-73130	Sequence 2130, App
C 430	18.4	0.7	60	1	PCT-US02-34777-2001	Sequence 2001, App
C 431	18.4	0.7	60	9	US-10-283-017-2001	Sequence 2001, App
C 432	18.4	0.7	60	9	US-10-316-957-2037	Sequence 2037, App
C 433	18.4	0.7	60	9	US-10-316-957-2037	Sequence 2037, App
C 434	18.4	0.7	60	9	US-10-328-624-1803	Sequence 1803, App
C 435	18.4	0.7	60	10	US-09-861-861-2073	Sequence 14629, App
C 436	18.2	0.7	25	6	US-09-866-108A-14629	Sequence 14629, App
C 437	18.2	0.7	25	9	US-10-098-263B-72773	Sequence 72773, App
C 438	18.2	0.7	25	9	US-10-355-577-8618	Sequence 8618, App
C 439	18.2	0.7	25	9	US-10-355-577-68083	Sequence 68083, App
C 440	18.2	0.7	25	9	US-10-355-577-134078	Sequence 134078, App
C 441	18.2	0.7	25	9	US-10-355-577-667474	Sequence 667474, App
C 442	18.2	0.7	25	11	US-10-355-577-911173	Sequence 911173, App
C 443	18.2	0.7	25	11	US-60-417-190-10219	Sequence 10219, App
C 444	18.2	0.7	25	11	US-60-427-808-8554	Sequence 8554, App
C 445	18.2	0.7	25	11	US-60-427-808-142837	Sequence 142837, App
C 446	18.2	0.7	25	11	US-60-427-808-380478	Sequence 380478, App
C 447	18.2	0.7	25	11	US-60-427-808-388921	Sequence 388921, App
C 448	18.2	0.7	25	11	US-60-427-808-441012	Sequence 441012, App
C 449	18.2	0.7	25	11	US-60-427-808-446174	Sequence 446174, App
C 450	18.2	0.7	25	11	US-60-427-808-484559	Sequence 484559, App
C 451	18.2	0.7	25	11	US-60-427-808-820371	Sequence 820371, App
C 452	18.2	0.7	25	11	US-60-427-808-876209	Sequence 876209, App
C 453	18.2	0.7	25	11	US-60-427-808-928659	Sequence 928659, App
C 454	18.2	0.7	25	11	US-60-427-808-954464	Sequence 954464, App
C 455	18.2	0.7	25	11	US-60-427-836-2417	Sequence 2417, App
C 456	18.2	0.7	25	11	US-60-427-836-36192	Sequence 36192, App
C 457	18.2	0.7	25	11	US-60-427-836-45498	Sequence 45498, App
C 458	18.2	0.7	25	11	US-60-427-836-51821	Sequence 51821, App
C 459	18.2	0.7	25	11	US-60-427-836-101761	Sequence 101761, App
C 460	18.2	0.7	25	11	US-60-427-836-118718	Sequence 118718, App
C 461	18.2	0.7	25	11	US-60-427-836-140646	Sequence 140646, App
C 462	18.2	0.7	25	11	US-60-427-836-157546	Sequence 157546, App
C 463	18.2	0.7	25	11	US-60-427-836-186844	Sequence 186844, App
C 464	18.2	0.7	25	11	US-60-427-836-219951	Sequence 219951, App
C 465	18.2	0.7	25	11	US-60-427-836-306970	Sequence 306970, App
C 466	18.2	0.7	25	11	US-60-427-836-311382	Sequence 311382, App
C 467	18.2	0.7	25	11	US-60-427-836-402469	Sequence 402469, App
C 468	18.2	0.7	25	11	US-60-427-836-429756	Sequence 429756, App
C 469	18.2	0.7	25	11	US-60-427-836-446242	Sequence 446242, App
C 470	18.2	0.7	25	11	US-60-427-836-456394	Sequence 456394, App
C 471	18.2	0.7	25	11	US-60-427-836-499317	Sequence 499317, App
C 472	18.2	0.7	39	6	US-09-548-797B-149	Sequence 589418, App
C 473	18.2	0.7	41	9	US-10-277-216-253	Sequence 149, App
C 474	18.2	0.7	45	6	US-09-904-196B-6	Sequence 253, App
C 475	18.2	0.7	45	6	US-10-318-966-6	Sequence 6, App1
C 476	18.2	0.7	46	6	US-09-989-733-239	Sequence 6, App1
C 477	18.2	0.7	46	6	US-09-992-643-239	Sequence 239, App
C 478	18.2	0.7	47	5	US-09-749-2808-2696	Sequence 2696, App
C 479	18.2	0.7	47	9	US-10-294-934-583	Sequence 583, App
C 480	18.2	0.7	47	9	US-10-349-143-632	Sequence 632, App
C 481	18.2	0.7	47	9	US-10-349-143-638	Sequence 638, App
C 482	18.2	0.7	47	9	US-10-349-143-1509	Sequence 1509, App
C 483	18.2	0.7	47	9	US-10-389-048-10096	Sequence 3785, App
C 484	18.2	0.7	48	8	US-10-405-666-68	Sequence 68, App1
C 485	18.2	0.7	48	8	US-10-409-627-194	Sequence 194, App
C 486	18.2	0.7	48	8	US-10-261-159A-74	Sequence 24, App1
C 487	18.2	0.7	48	8	US-09-749-2808-7403	Sequence 603, App
C 488	18.2	0.7	50	5	US-09-912-293-62813	Sequence 7415, App
C 489	18.2	0.7	50	6	US-10-325-899-184	Sequence 184, App
C 490	18.2	0.7	50	6	US-10-325-899-630	Sequence 630, App
C 491	18.2	0.7	50	9	US-10-325-899-1404	Sequence 1404, App
C 492	18.2	0.7	50	9	US-10-325-899-2467	Sequence 2467, App
C 493	18.2	0.7	50	9	US-10-325-899-2862	Sequence 2862, App
C 494	18.2	0.7	50	9	US-10-325-899-3074	Sequence 3074, App
C 495	18.2	0.7	50	9	US-10-325-899-3370	Sequence 3370, App
C 496	18.2	0.7	50	9	US-10-325-899-4502	Sequence 4502, App
C 497	18.2	0.7	50	9	US-10-325-899-4742	Sequence 4742, App
C 500	18.2	0.7	50	9	US-10-325-899-4742	Sequence 4742, App

ALIGNMENTS

RESULT 1

US-09-749-2808-127 Application US/09749280B

GENERAL INFORMATION:

APPLICANT: Shinketsu, Richard A.

TITLE OF INVENTION: Nucleic Acids Containing Single

FILE REFERENCE: 15966-610

CURRENT APPLICATION NUMBER: US/09/749, 2808

PRIOR FILING DATE: 2000-12-27

PRIOR APPLICATION NUMBER: 60/173,419

NUMBER OF SEQ ID NOS: 10038

SOFTWARE: Curagen Patent Formatter Version 0.9

SEQ ID NO 127

LENGTH: 51

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: allele

LOCATION: (26)..(0)

OTHER INFORMATION: single nucleotide polymorphism

FEATURE:

NAME/KEY: misc.feature

LOCATION: (0)..(0)

OTHER INFORMATION: Accession number cg44031583

US-09-749-2808-127

;; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
;; FILE REFERENCE: 109845.158
;; CURRENT APPLICATION NUMBER: PCT/US03/02358
;; CURRENT FILING DATE: 2003-01-23
;; PRIOR APPLICATION NUMBER: US 10/057,408
;; PRIOR FILING DATE: 2002-01-23
;; NUMBER OF SEQ ID NOS: 87
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 36
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Partial zinc finger domain oligomer
;; NAME/KEY: misc_feature
;; LOCATION: (45)..(56)
;; OTHER INFORMATION: Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or c.
PCT-US03-02358-36

Query Match 1.0%; Score 27; DB 1; Length 60;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1593 GGGGAGAACCCATTGTATGTACGAGTGGGCGGCGGCTTTACCCGGAATCAACCCCTG.1652
Db 1 GGGGAGAACCCGCTATAATGTCGCGAATGTGCTAAAGTTTACGNNNAGCNNNNNTTG 50

RESULT 6
US-09-911-261B-36
;; Sequence 36, Application US/09911261B
;; GENERAL INFORMATION:
;; APPLICANT: Sera, Takashi
;; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
;; FILE REFERENCE: 109845.135
;; CURRENT APPLICATION NUMBER: US/09/911,261B
;; CURRENT FILING DATE: 2000-07-21
;; PRIOR APPLICATION NUMBER: US 60/220,060
;; PRIOR FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 69
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 36
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Partial zinc finger domain oligomer
;; NAME/KEY: misc_feature
;; LOCATION: (45)..(56)
;; OTHER INFORMATION: Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or c.
US-09-911-261B-36

Query Match 1.0%; Score 27; DB 5; Length 60;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1593 GGGGAGAACCCATTGTATGTACGAGTGGGCGGCGGCTTTACCCGGAATCAACCCCTG 1652
Db 1 GGGGAGAACCCGCTATAATGTCGCGAATGTGCTAAAGTTTACGNNNAGCNNNNNTTG 60

RESULT 7
US-09-911-261A-36
;; Sequence 36, Application US/09911261A
;; GENERAL INFORMATION:
;; APPLICANT: Sera, Takashi
;; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
;; FILE REFERENCE: 109845.135
;; CURRENT APPLICATION NUMBER: US/09/911,261A
;; CURRENT FILING DATE: 2001-07-23
;; PRIOR APPLICATION NUMBER: US 60/220,060

;; PRIOR FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 69
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 36
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Partial zinc finger domain oligomer
;; NAME/KEY: misc_feature
;; LOCATION: (45)..(56)
;; OTHER INFORMATION: Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or c.
US-09-911-261A-36

Query Match 1.0%; Score 27; DB 6; Length 60;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1593 GGGGAGAACCCATTGTATGTACGAGTGGGCGGCGGCTTTACCCGGAATCAACCCCTG 1652
Db 1 GGGGAGAACCCGCTATAATGTCGCGAATGTGCTAAAGTTTACGNNNAGCNNNNNTTG 60

RESULT 8
US-09-749-280B-5554
;; Sequence 5554, Application US/09749280B
;; GENERAL INFORMATION:
;; APPLICANT: Shimkets, Richard A.
;; TITLE OF INVENTION: Nucleic Acids Containing Single
;; FILE REFERENCE: 15966-610
;; CURRENT APPLICATION NUMBER: US/09/749,280B
;; CURRENT FILING DATE: 2000-12-27
;; PRIOR APPLICATION NUMBER: 60/173,419
;; PRIOR FILING DATE: 1999-12-28
;; NUMBER OF SEQ ID NOS: 10038
;; SOFTWARE: Curagen Patent Formatter Version 0.9
;; SEQ ID NO 5554
;; LENGTH: 51
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: (26)..(0)
;; OTHER INFORMATION: single nucleotide polymorphism
;; NAME/KEY: misc_feature
;; LOCATION: (0)..(0)
;; OTHER INFORMATION: Accession number c943959535
US-09-749-280B-5554

Query Match 1.0%; Score 26.8; DB 5; Length 51;
Best Local Similarity 73.9%; Pred. No. 3.1e+03;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 214 TGGCATTCAGGATGTGCTGTACTTACCCGAGGAGGTGAG 259
Db 1 TGACTTTGAAGACGTGCTGTGTAATTTCCAGGAGATGAG 46

RESULT 9
US-09-749-280B-6407
;; Sequence 6407, Application US/09749280B
;; GENERAL INFORMATION:
;; APPLICANT: Shimkets, Richard A.
;; TITLE OF INVENTION: Nucleic Acids Containing Single
;; FILE REFERENCE: 15966-610
;; CURRENT APPLICATION NUMBER: US/09/749,280B
;; CURRENT FILING DATE: 2000-12-27

```
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 6407
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43051067
; US-09-749-280B-6407

Query Match
Best Local Similarity 1.0%; Score 26.8; DB 5; Length 51;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1560 TCAAACTTAAACAACACGAGGTCAACACAGGGGAGAGCCAT 1605
Db 1 TCAAACTGACATCCACGACGAGAACACACAGGAGAGGCCCT 46

RESULT 10
PCT-US03-02358-49
; Sequence 49, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.158
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
PCT-US03-02358-49

Query Match
Best Local Similarity 1.0%; Score 26.6; DB 1; Length 56;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 921 GGGAGACACCTTACATGTACAGTGGGAGAGACAGCTTTGGCAGTA 969
Db 1 GGGAGAAAGCCTTACAGTGGCCGTGAATGCGGAAAGACCTTTAGTCGTA 49

RESULT 11
US-09-911-261B-49
; Sequence 49, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261B
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 56
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-49

Query Match
Best Local Similarity 1.0%; Score 26.6; DB 5; Length 56;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 921 GGGAGACACCTTACATGTACAGTGGGAGAGACAGCTTTGGCAGTA 969
Db 1 GGGAGAAAGCCTTACAGTGGCCGTGAATGCGGAAAGACCTTTAGTCGTA 49

RESULT 12
US-09-911-261A-49
; Sequence 49, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-49

Query Match
Best Local Similarity 1.0%; Score 26.6; DB 6; Length 56;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 921 GGGAGACACCTTACATGTACAGTGGGAGAGACAGCTTTGGCAGTA 969
Db 1 GGGAGAAAGCCTTACAGTGGCCGTGAATGCGGAAAGACCTTTAGTCGTA 49

RESULT 13
PCT-US03-02358-45
; Sequence 45, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.158
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
PCT-US03-02358-45

Query Match
Best Local Similarity 0.9%; Score 25.8; DB 1; Length 60;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1593 GGGAGAAAGCATTGTATGTACGAGTGGGCGAGGCGCTTTACC 1637
Db 1 GGGAGAAAGCCGTATTAATGTCGGAATGTGTAAGTTTACG 45
```

```
RESULT 14
US-09-911-261B-45
; Sequence 45, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261B
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-45
```

```
Query Match          0.9%; Score 25.8; DB 5; Length 60;
Best Local Similarity 73.3%; Pred. No. 6.4e+03;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
OY      1593 GGGGAGAACCCATTGTGTATGACGAGTGTGGCGAGCCTTTACC 1637
DB      1 GGGGAGAACCCGCTATAATGTCGGAATGTGTAAGTTTACG 45
|||||
```

```
RESULT 15
US-09-911-261A-45
; Sequence 45, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-45
```

```
Query Match          0.9%; Score 25.8; DB 6; Length 60;
Best Local Similarity 73.3%; Pred. No. 6.4e+03;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
OY      1593 GGGGAGAACCCATTGTGTATGACGAGTGTGGCGAGCCTTTACC 1637
DB      1 GGGGAGAACCCGCTATAATGTCGGAATGTGTAAGTTTACG 45
|||||
```

```
RESULT 16
PCT-US03-02358-40
; Sequence 40, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.138
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (48)..(58)
; OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or
PCT-US03-02358-40
```

```
Query Match          0.9%; Score 25.6; DB 1; Length 56;
Best Local Similarity 72.1%; Pred. No. 7.1e+03;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
OY      1179 AAGCCTTATGTGTGCAAGCAATGTGGCAGACCTTTAGCCTGA 1221
DB      7 AAGCCTTACAGTGCCTCGATGCGGAGAGACCTTTAGTNNNA 49
|||||
```

```
RESULT 17
US-09-911-261B-40
; Sequence 40, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261B
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (48)..(58)
; OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or
US-09-911-261B-40
```

```
Query Match          0.9%; Score 25.6; DB 5; Length 56;
Best Local Similarity 72.1%; Pred. No. 7.1e+03;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
OY      1179 AAGCCTTATGTGTGCAAGCAATGTGGCAGACCTTTAGCCTGA 1221
DB      7 AAGCCTTACAGTGCCTCGATGCGGAGAGACCTTTAGTNNNA 49
|||||
```

```
RESULT 18
US-09-911-261A-40
; Sequence 40, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48)..(58)
OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or c.
US-09-911-261A-40
```

```
Query Match      0.9%: Score 25.6; DB 6; Length 56;
Best Local Similarity 72.1%; Pred. No. 7.1e+03;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY      1179 AAGCCTTATGTGTCAGGAATGTGGCAGAGCTTTAGCCTGA 1221
          |||||  |||  |||||  |||||  |||||  |||||  |||||
Db       7 AAGCCTTACAAGTGCCTGATGCGGAGAGAGCTTAGTNNNA 49
```

```
RESULT 19
US-10-325-899-2511
Sequence 2511, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2511
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-899-2511
```

```
Query Match      0.9%: Score 25.2; DB 9; Length 50;
Best Local Similarity 71.7%; Pred. No. 8.9e+03;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY      1547 CTTAGCCTGAAGTCAACCTTAACAACACAGGTCACACAGC 1592
          |||||  |||  |||||  |||||  |||||  |||||  |||||
Db       4 CTTAGTCAGAGCTCAACCTTAGTCAACACAGGATTCACATG 49
```

```
RESULT 20
US-10-325-899-3660
Sequence 3660, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
```

```
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3660
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-899-3660
```

```
Query Match      0.9%: Score 25.2; DB 9; Length 50;
Best Local Similarity 71.7%; Pred. No. 8.9e+03;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY      1547 CTTAGCCTGAAGTCAACCTTAACAACACAGGTCACACAGC 1592
          |||||  |||  |||||  |||||  |||||  |||||  |||||
Db       4 CTTAGTCAGAGCTCAACCTTAGTCAACACAGGATTCACATG 49
```

```
RESULT 21
US-09-749-280B-519
Sequence 519, Application US/09749280B
GENERAL INFORMATION:
APPLICANT: Shinkets, Richard A.
APPLICANT: Leach, Martin
TITLE OF INVENTION: Nucleic Acids Containing Single
FILE REFERENCE: 15966-610
CURRENT APPLICATION NUMBER: US/09/749,280B
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/173,419
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 10038
SOFTWARE: Curacen Patent Formatter Version 0.9
SEQ ID NO 519
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number c943051067
US-09-749-280B-519
```

```
Query Match      0.9%: Score 25.2; DB 5; Length 51;
Best Local Similarity 71.7%; Pred. No. 8.9e+03;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY      1225 CAACCTCATTTACCAACCAAGAGGCGCACACTGGGGAGAGCCTTA 1270
          |||||  |||  |||||  |||  |||||  |||||  |||||
Db       1 CAACCTGCACATCCACCAAGGAGTTTCACACAGAGAGGCCCTA 46
```

```
RESULT 22
PCT-US03-02358-50/c
Sequence 50, Application PC/TUS0302358
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845,158
CURRENT APPLICATION NUMBER: PCT/US03/02358
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US 10/057,408
PRIOR FILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
SEQ ID NO 50
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
```

PCT-US03-02358-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 1; Length 55;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1211 CTTAGCCTGAAGTCAACCTCATTACCCAGAGGGCGCACACTGGGAGAG 1265
DB 55 CTTAGTCGTAGTGATAGCTTACAAACCCAGCAGCAGCAGCGGAGAG 1

RESULT 23

US-09-911-261B-50/c
Sequence 50, Application US/0911261B
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845.135
CURRENT APPLICATION NUMBER: US/09/911,261B
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 5; Length 55;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1211 CTTAGCCTGAAGTCAACCTCATTACCCAGAGGGCGCACACTGGGAGAG 1265
DB 55 CTTAGTCGTAGTGATAGCTTACAAACCCAGCAGCAGCAGCGGAGAG 1

RESULT 24

US-09-911-261A-50/c
Sequence 50, Application US/0911261A
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845.135
CURRENT APPLICATION NUMBER: US/09/911,261A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 6; Length 55;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1211 CTTAGCCTGAAGTCAACCTCATTACCCAGAGGGCGCACACTGGGAGAG 1265
DB 55 CTTAGTCGTAGTGATAGCTTACAAACCCAGCAGCAGCAGCGGAGAG 1

RESULT 25

US-09-749-280B-5867

Sequence 5867, Application US/09749280B

GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Nucleic Acids Containing Single
TITLE OF INVENTION: Nucleic Acids Containing Single
FILE REFERENCE: 15966-610
CURRENT APPLICATION NUMBER: US/09/749,280B
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/173,419
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 10038
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 5867
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number c942532030
US-09-749-280B-5867

Query Match
Best Local Similarity 0.9%; Score 24.4; DB 5; Length 51;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1353 TACATTGCGAGGAGTGTGAGCAGGCTTTACCCAGAGTCAACCTCAT 1402
DB 1 TATAATGTGATGAGTGTGCGAAGCTTCACTCAGAGCTCATCTTAT 50

RESULT 26

US-09-749-280B-6408
Sequence 6408, Application US/09749280B
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Nucleic Acids Containing Single
TITLE OF INVENTION: Nucleotide Polymorphisms and Methods of Use Thereof
FILE REFERENCE: 15966-610
CURRENT APPLICATION NUMBER: US/09/749,280B
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/173,419
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 10038
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 6408
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number c943051067
US-09-749-280B-6408

Query Match
Best Local Similarity 0.9%; Score 24.4; DB 5; Length 51;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1548 TTTAGCCTGAAGTCAACCTTACCAACACGAGGCTGACACAGGGGGA 1597
DB 1 TTACAGCAGAGCTCCACCTTACAGCCAGCAGCGGCTTCAAGAAAGA 50

RESULT 27
PCT-US03-02358-41/c
; Sequence 41, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.158
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (28)..(48)
; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" =
; OTHER INFORMATION: g, a, t, or c
PCT-US03-02358-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 1; Length 55;
Best Local Similarity 56.4%; Pred. No. 2.4e+04;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCCTGAAGTCAACCTTAACAACACAGAGTCACACACGGGGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACAAANNNCACACGACGACGAGGAGAG 1

RESULT 28
US-09-911-261B-41/c
; Sequence 41, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911.261B
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (28)..(48)
; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" =
; OTHER INFORMATION: g, a, t, or c
US-09-911-261B-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 5; Length 55;
Best Local Similarity 56.4%; Pred. No. 2.4e+04;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCCTGAAGTCAACCTTAACAACACAGAGTCACACACGGGGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACAAANNNCACACGACGACGAGGAGAG 1

RESULT 29
US-09-911-261A-41/c

; Sequence 41, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911.261A
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (28)..(48)
; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" =
; OTHER INFORMATION: g, a, t, or c
US-09-911-261A-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 6; Length 55;
Best Local Similarity 56.4%; Pred. No. 2.4e+04;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCCTGAAGTCAACCTTAACAACACAGAGTCACACACGGGGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACAAANNNCACACGACGACGAGGAGAG 1

RESULT 30
US-10-310-156A-470/c
; Sequence 470, Application US/10310156A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Chlamydomophila pneumoniae AR39, complete genome.
; FILE REFERENCE: Jim Zegeer law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/310.156A
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Proprietary
; SEQ ID NO 470
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Chlamydomophila pneumoniae AR39, complete genome.
; FEATURE:
; LOCATION: (827553)...(827610)
; OTHER INFORMATION: Chromosome = 1 strand = positive ConnectonObjectNumber =
US-10-310-156A-470

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 8; Length 58;
Best Local Similarity 80.0%; Pred. No. 2.4e+04;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2274 CTTGAGGAGATTCCTGCTCATTTTCAGGAGCC 2308
Db 39 CTTGAGGAGTTCCTGCTCCTCTCTGAGAGCC 5

RESULT 31
US-10-310-156-470/c
; Sequence 470, Application US/10310156
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Chlamydomophila pneumoniae AR39, complete genome.
; FILE REFERENCE: Jim Zegeer law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/310.156
; PRIOR FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Proprietary


```

; SEQ ID NO 470
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Chlamydomophila pneumoniae AR39, complete genome.
; FEATURE:
; LOCATION: (827553)..(827610)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-310-156-470
ConnectronObjectNumber = 58

```

Query Match	0.9%	Score 23.8	DB 9	Length 58
Best Local Similarity	80.0%	Pred. No. 2.4e+04		
Matches 28; Conservative	0	Mismatches 7	Indels 0	Gaps 0

QY 2274 CCTGAGGAGGAATTCCTGGCTCAATTTTCTAGGAGCC 2308
||||||| | ||||||| || |||||||
Db 39 CCTGAGGAGGTTTTCGCTGGCTCCCTTCTAGGAGCC 5

```

RESULT 32
US-09-912-293-732/c
: Sequence 732, Application US/09912293
: GENERAL INFORMATION:
: APPLICANT: Rosen, et. al.
: TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
: FILE REFERENCE: Pd-100
: CURRENT APPLICATION NUMBER: US/09/912,293
: PRIOR FILING DATE: 2001-07-26
: PRIOR APPLICATION NUMBER: 08/103,744
: PRIOR FILING DATE: 1993-08-09
: PRIOR APPLICATION NUMBER: 09/249,651
: PRIOR FILING DATE: 1999-02-12
: PRIOR APPLICATION NUMBER: 08/104,507
: PRIOR FILING DATE: 1993-08-09
: PRIOR APPLICATION NUMBER: 08/196,363
: PRIOR FILING DATE: 1994-02-15
: PRIOR APPLICATION NUMBER: 09/859,490
: PRIOR FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: 08/196,362
: PRIOR FILING DATE: 1994-02-15
: PRIOR APPLICATION NUMBER: 08/221,623
: PRIOR FILING DATE: 1994-03-31
: PRIOR APPLICATION NUMBER: 08/220,691
: PRIOR FILING DATE: 1994-03-31
: PRIOR APPLICATION NUMBER: 09/741,830
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 09/813,155
: PRIOR FILING DATE: 2001-03-21
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 244558
: SEQ ID NO 732

```

Query Match	0.88;	Score 23;	DB 6;	Length 59;
Best Local Similarity	62.78;	Pred. No. 4.2e+04;		

Matches	32;	Conservative	0;	Mismatches	19;	Indels	0;	Gaps	0
QY	2596	ACTTACAATCAGTCACGTGATTCCTATTCGTGAGCCCTATAAAGCC	2646						
Db	51	ATTCAATTCGNCANCATTTNGTCCTCATTCCTCATATCAAGAACGCC	1						

```

RESULT 33
US-60-449-155-516
: Sequence 516, Application US/60449155
: GENERAL INFORMATION:
: APPLICANT: Kelly, Tim
: TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
: TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES A
: FILE REFERENCE: HUMO2-11P
: CURRENT APPLICATION NUMBER: US/60/449,155
: CURRENT FILING DATE: 2003-02-20
: NUMBER OF SEQ ID NOS: 1000
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 516
: LENGTH: 41
: TYPE: DNA
: ORGANISM: Human
US-60-449-155-516

```

Query Match	0.8%	Score 22.4	DB 11	Length 41
Best Local Similarity	72.5%	Pred. No. 5.3e+04		
Matches 29	Conservative 0	Mismatches 11	Indels 0	Gaps 0

```

QY      2061 AACCTTATCAGACATCAGAGGACACACACTCAGATGAAAC 2100
          | | | | | | | | | | | | | | | | | | | |
Db      2   ACCCTTATCGAACATCAGGGAATTACACACTGGACAAAAC 41

```

```

RESULT 34
PCT-US03-02358-39/C
? Sequence 39, Application PC/TUS0302358
? GENERAL INFORMATION:
? APPLICANT: Sera, Takashi
? FILE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
? TITLE REFERENCE: 109845,158
? CURRENT APPLICATION NUMBER: PCT/US03/02358
? CURRENT FILING DATE: 2003-01-23
? PRIOR APPLICATION NUMBER: US 10/057,408
? PRIOR FILING DATE: 2002-01-23
? NUMBER OF SEQ ID NOS: 87
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 39
? LENGTH: 60
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Partial zinc finger domain oligomer
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (37)..(51)
? OTHER INFORMATION: Nucleotides 37-39 and 46-51 are "n" wherein "n" = g,
? CTT-US03-02358-39

```

Query Match	0.88;	Score 22.4;	DB 1;	Length 60;
Best Local Similarity	81.28;	Pred. No. 6.3e+04;		
Matches 26; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0

QY 1239 CACCAGAGGGGGCACACTGGGGAGAGACCTTA 1270
 ||||| | ||||| |||||
 Db 36 CACACGCTACTCACACTGGGGAGAGACCTTA 5

```
RESULT 35
PCT-0503-02358-48/c
; Sequence 48, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
```

```

: TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
: FILE REFERENCE: 109845.158
: CURRENT APPLICATION NUMBER: PCT/US03/02358
: CURRENT FILING DATE: 2003-01-23
: PRIOR APPLICATION NUMBER: US 10/057,408
: PRIOR FILING DATE: 2002-01-23
: NUMBER OF SEQ. ID NOS.: 87
: SOFTWARE: PatentIn version 3.2
: SEQ. ID NO 48
: LENGTH: 60
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Partial zinc finger domain oligomer
PCT-US03-02358-48

```

	0.8%;	Score 22.4;	DB 1;	length 60;
Query Match	Best Local Similarity	81.2%;	Pred. No. 6.3e+04;	
Matches	26; Conservative	0; Mismatches	6; Indels	0; Gaps
QY	1239 CACCGAGGGGCGACACTGGGGAGAGGCCTTA	1270		
Dd	36 CATCAGCGTACTCACACTGGCGGAGAGGCCTTA	5		

```

RESULT 36
US-09-911-261B-39/C
: Sequence 39, Application US/09911261B
: GENERAL INFORMATION:
: APPLICANT: Serz, Takashi
: TITLE OF INVENTION: zinc finger Domain Recognition Code and Uses Thereof
: FILE REFERENCE: 109845.135
: CURRENT APPLICATION NUMBER: US/09/911,261B
: CURRENT FILING DATE: 2000-07-21
: PRIORITY APPLICATION NUMBER: US 60/220,060
: PRIORITY FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 39
: LENGTH: 60
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Partial zinc finger domain oligomer
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (37)-(51)
: OTHER INFORMATION: Nucleotides 37-39 and 46-51 are "n" wherein "n" = g, a, t, or c.
US-09-911-261B-39

```

```

Query Match          0.8%; Score 22.4; DB 5; Length 60;
Best Local Similarity 81.2%; Pred. No. 6.3e+04;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps

QY      1239 CACCAGAGGGCGGCACACTCTGGGAGAACCTTA 1270
          || ||| | | | | | | | | | | | | | | | | |
Db       36 CATCAGCGTACTCATCAGCTGGCGAGAGCCTTA 5

RESULT 37
US-09-911-261B-48/c
: Sequence 48, Application US/09911261B
: GENERAL INFORMATION:
: APPLICANT: Sera, Takashi
: TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
: FILE REFERENCE: 109845.135
: CURRENT APPLICATION NUMBER: US/09/911,261B
: CURRENT FILING DATE: 2000-07-21
: PRIOR APPLICATION NUMBER: US 60/220,060
: PRIOR FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: Patent version 3.0
: SEQ ID NO 48

```

```

: LENGTH: 60
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-48

```

Query Match	0.88;	Score 22.4;	DB 5;	Length 60;
Best Local Similarity	81.28;	Pred. No. 6.3e+04;		
Matches	26;	Conservative	0;	Mismatches 6;
			Indels	0;
			Gaps	0;

Qy 1239 CACCAGAGGGGGCACCACCTGGGAGAGACCTTA 1270
 ||||| | ||||| ||||| |||||
 Db 36 CATCAGCGTACTCACACTGGCGAGAGAAGCCTTA 5

```

RESULT 38
US-09-911-261A-39/c
; Sequence 39, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (37)-(51)
; OTHER INFORMATION: Nucleotides 37-39 and 46-51 are "n" wherein "n" = g, a, t, or
US-09-911-261A-39

```

```

OY      1239 CACCACAGGGCGCACACTGTGGGAGAAGCCTTA 1270
          ||| | | | | | | | | | | | | | | | | | | |
Db       36 CATCAGCGTACTCACACTGGCGAGAGCCCTTA 5

RESULT 39
US-09-911-261A-48/c
Sequence 48, Application US/09911261A
GENERAL INFORMATION:
APPLICANT: Seta, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845.135
CURRENT APPLICATION NUMBER: US/09/911,261A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.0
SEQ ID NO 48
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-48

Query Match      0.8%; Score 22.4; DB 6; Length 60;
Best Local Similarity 81.2%; Pred. No. 6.3e+04;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps

```

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1239 CACCAGAGCCGACACTGGGAGAACCTTA 1270
DB 36 CATCAGCTACTCAGACTGGCAGAGACCTTA 5

RESULT 40

US-09-749-280B-6410
; Sequence 6410, Application US/09749280B
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single
; FILE REFERENCE: 15966-610
; CURRENT APPLICATION NUMBER: US/09/749,280B
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 6410
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg42532030
US-09-749-280B-6410

Query Match

Best Local Similarity 64.7%; Score 22.2; DB 5; Length 51;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 1184 TTATGTGTCAGCAAGATGTGGCAGAGCTTTAGCCTGAGTCACCAACCTCAT 1234
DB 1 TTATTAATGTGATGATGAGTGTGGGAAACCTTCAGTACAGACTCAGATCTTAT 51

RESULT 41

US-60-427-808-134357
; Sequence 134357, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-134357

Query Match

Best Local Similarity 92.0%; Score 21.8; DB 11; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2146 ACTTCATGACAGCAGGAGGACACA 2170
DB 1 ACTTCATGACAGCAGGAGGACACA 25

RESULT 42

US-60-427-836-480873

; Sequence 480873, Application US/60427836

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 480873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-480873

Query Match

Best Local Similarity 92.0%; Score 21.8; DB 11; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 236 GTACTTCACCCAGAGAGTGAGG 260
DB 1 GTACTTCACCCAGAGAGTGAGG 25

RESULT 43

US-60-449-155-517
; Sequence 517, Application US/60449155
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; FILE REFERENCE: HUM02-11P
; CURRENT APPLICATION NUMBER: US/60/449,155
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 1000
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Human
US-60-449-155-517

Query Match

Best Local Similarity 70.7%; Score 21.8; DB 11; Length 41;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1348 AACCTTACATTTGCGAGGAGTGTGAGCAAGCCTTAGCCAG 1388
DB 1 AACCTTACATTTGCGAGGAGTGTGAGCAAGCCTTAGCCAG 41

RESULT 44

PCT-US03-11497-11
; Sequence 11, Application PC/TUS0311497
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
; FILE REFERENCE: 160 200 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/11497
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,669
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,882
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/424,336
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/374,823
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/376,558
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/381,366
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/403,648

PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US03-11497-11

Query Match
Best Local Similarity 65.3%; Score 21.8; DB 1; Length 50;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1980 CTCATTAGACACAGAGACACATTCAGAGAGAAAGCCTTATATTGCA 2028
DB 2 CTCCTTAGATATAAAGGCGACATTTATTAAGAACCCGATTATATCA 50

RESULT 45
US-10-257-848-81/c
Sequence 81, Application US/10257848
GENERAL INFORMATION:

APPLICANT: ITOH, Yasuaki
APPLICANT: SUZUKI, Nobuhiro
APPLICANT: NISHI, Kazunori
APPLICANT: KIZAWA, Hideki
APPLICANT: HARADA, Masataka
APPLICANT: OGI, Kazuhiro
TITLE OF INVENTION: Novel Insulin/IGF/Relaxin Family Polypeptide and Its DNA
FILE REFERENCE: 2717 USOP
CURRENT APPLICATION NUMBER: US/10/257,848
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: PCT/JPOL/03399
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: JP 12-126340
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: JP 12-205587
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: JP 12-247962
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: JP 12-395050
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 81
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: for peptide
US-10-257-848-81

Query Match
Best Local Similarity 65.3%; Score 21.8; DB 9; Length 60;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 577 ATCCAGAGATGAGAAACAGAGATTCATCTCTTGTAGTGGCAA 625
DB 58 ACCCATACCGCCAGAGAGACAGACATGATCTTGCATGCTGCA 10

RESULT 46
US-10-325-899-4332/c
Sequence 4332, Application US/10325899
GENERAL INFORMATION:

APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
FILE REFERENCE: 50661200012
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4332
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-899-4332

Query Match
Best Local Similarity 75.0%; Score 21.6; DB 9; Length 50;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 888 TCMAACCTCCTTAGCCTCCGAGAGACAACTGGG 923
DB 47 TTAACATCCCTAGCCCTTACCAAGGCACCAAGCGG 12

RESULT 47
US-09-749-280B-5462/c
Sequence 5462, Application US/09749280B
GENERAL INFORMATION:

APPLICANT: Shinkets, Richard A.
APPLICANT: Leach, Martin
TITLE OF INVENTION: Nucleic Acids Containing Single
FILE REFERENCE: 15966-610
CURRENT APPLICATION NUMBER: US/09/749,280B
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/173,419
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 10038
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 5462
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:
NAME/KEY: misc_feature
LOCATION: (25)...(26)
OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number. cg44911411
US-09-749-280B-5462

Query Match
Best Local Similarity 71.8%; Score 21.4; DB 5; Length 50;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1522 ATGCTGCTGAGTGGGCGAGTGTTCAGCTGAAGT 1560
DB 50 AGGACTGCGCTGATTTGGGGCAGGCTAGACCCGGAGT 12

RESULT 48
US-10-325-899-4844/c
Sequence 4844, Application US/10325899
GENERAL INFORMATION:

APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
; FILE REFERENCE: REJECTION
; CURRENT APPLICATION NUMBER: US/10/325, 899.
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4844
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-325-899-4844
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Query Match          0.8%; Score 21.4; DB 9; Length 50;
Best Local Similarity 71.8%; Pred. No. 1.1e+05;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY      2632 AGCCCATAAAGACCCAGACTGCTGAGTGAGAGAG 2670
Db      39 AACCAAAACATCAGACAGACTCAGCAGCAGTGGGAGGC 1
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RESULT 49
US-09-749-280B-1151/c
; Sequence 1151, Application US/09749280B
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single
; FILE REFERENCE: 15966-610
; CURRENT APPLICATION NUMBER: US/09/749,280B
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 1151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; NAME/KEY: misc_feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg42924171
; US-09-749-280B-1151
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Query Match          0.8%; Score 21.2; DB 5; Length 50;
Best Local Similarity 76.5%; Pred. No. 1.3e+05;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY      171 AAATGGCTACGAGGCTCTCTGAGAGCCAAAG 204
Db      34 AAATGCTTCCAGGCTCTCTGAGAGCCAGAGC 1
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RESULT 50
US-10-089-560-10/c
; Sequence 10, Application us/10089560
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; GENERAL INFORMATION:
; APPLICANT: Straume, Tore
; TITLE OF INVENTION: Particle Analysis Assay for Biomolecular Quantification
; FILE REFERENCE: 1321.2.71
; CURRENT APPLICATION NUMBER: US/10/089,560
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/158,664
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-10-089-560-10
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Query Match          0.8%; Score 21.2; DB 8; Length 50;
Best Local Similarity 64.0%; Pred. No. 1.3e+05;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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QY      1592 GGGGGAGAGCCATTGTATGTACGAGTGTGGCGGAGCTTTACCGGA 1641
Db      50 GTGGAAGATGCCCTTTGAAGCAGCATGGGCTTGGGTAGATTGTCCTGA 1
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Search completed: June 4, 2003, 12:40:27
Job time : 1950 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 09:21:00 ; Search time 6053 Seconds
(without alignments)
11514.121 Million cell updates/sec

Title: US-09-898-556A-3
Perfect score: 2772
Sequence: 1 caggcgcttaagctggttg.....ttctaccatccaccct 2772

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

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Result No.	Score	Query Match	Length	DB ID	Description
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3	60	2.2	60	72	US-60-287-724-6782
4	51	1.8	51	61	US-60-172-373-18031
5	51	1.8	51	61	US-60-172-373-18032
6	49.4	1.8	51	28	US-09-718-321A-465
7	49.4	1.8	51	28	US-09-718-321A-465
8	49.4	1.8	51	61	US-60-172-373-18033
9	49.4	1.8	51	71	US-60-278-258-5294
10	49.4	1.8	51	71	US-60-278-258-5296
11	49.4	1.8	51	71	US-60-278-258-5297
12	49.4	1.8	51	76	US-60-324-185-24475
13	47.8	1.7	51	76	US-60-324-185-24475
14	41.4	1.5	51	76	US-60-324-185-4221
15	40.4	1.5	51	65	US-60-213-359-20
16	39.8	1.4	51	67	US-60-234-690-1769
17	38.2	1.4	51	76	US-60-324-185-1769
18	38.2	1.4	51	76	US-60-324-185-1769
19	35.6	1.3	51	65	US-60-213-359-2531
20	35	1.3	51	65	US-60-213-359-2531
21	35	1.3	60	34	US-09-908-975-6663

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22	35	1.3	60	34	US-09-908-975A-6663	Sequence 6663, Ap	95	29.4	1.1	51	76	US-60-324-185-30556	Sequence 30556, A
23	35	1.3	60	72	US-60-287-724-6663	Sequence 6663, Ap	96	29.2	1.1	51	61	US-60-172-373-5372	Sequence 5372, Ap
24	34.6	1.2	51	29	US-09-726-173A-4584	Sequence 4584, Ap	97	29.2	1.1	51	71	US-60-278-258-5820	Sequence 5820, Ap
25	33.6	1.2	51	76	US-60-324-185-4342	Sequence 4342, Ap	98	29.2	1.1	51	76	US-60-324-185-3755	Sequence 3755, Ap
26	33.4	1.2	51	61	US-60-172-360-29152	Sequence 29152, A	99	29.2	1.1	51	76	US-60-324-185-3755	Sequence 3755, Ap
27	33.4	1.2	51	76	US-60-250-830-1043	Sequence 1043, Ap	100	29.2	1.1	51	71	US-60-278-258-5820	Sequence 5820, Ap
28	33.4	1.2	51	76	US-60-323-966-1043	Sequence 1043, Ap	101	29.2	1.1	51	71	US-60-324-185-3946	Sequence 3946, Ap
29	33	1.2	51	29	US-09-726-173A-4583	Sequence 4583, Ap	102	28.8	1.0	51	65	US-60-213-360-2930	Sequence 2930, Ap
30	32.6	1.2	51	61	US-60-172-373-5373	Sequence 5373, Ap	103	28.8	1.0	51	65	US-60-213-360-2930	Sequence 2930, Ap
31	32.6	1.2	51	65	US-60-213-360-2773	Sequence 2773, Ap	104	28.8	1.0	51	71	US-60-278-258-5866	Sequence 5866, Ap
32	32.4	1.2	51	76	US-60-278-258-5877	Sequence 5877, Ap	105	28.8	1.0	51	71	US-60-278-258-5866	Sequence 5866, Ap
33	32.4	1.2	51	76	US-60-324-185-4224	Sequence 4224, Ap	106	28.6	1.0	51	76	US-60-323-966-992	Sequence 992, Ap
34	32.4	1.2	51	76	US-60-324-185-6741	Sequence 6741, Ap	107	28.6	1.0	51	65	US-60-213-359-317	Sequence 317, Ap
35	32	1.2	51	65	US-60-213-359-1622	Sequence 1622, Ap	108	28.6	1.0	51	65	US-60-213-360-2944	Sequence 2944, Ap
36	32	1.2	51	65	US-60-213-360-2926	Sequence 2926, Ap	109	28.6	1.0	51	65	US-60-213-360-2944	Sequence 2944, Ap
37	32	1.2	51	76	US-60-250-830-822	Sequence 822, App	110	28.6	1.0	51	69	US-60-250-830-1031	Sequence 1031, Ap
38	32	1.2	51	69	US-60-323-966-822	Sequence 822, App	111	28.6	1.0	51	69	US-60-250-830-1090	Sequence 1090, Ap
39	31.8	1.1	51	61	US-60-172-373-5588	Sequence 5588, App	112	28.6	1.0	51	71	US-60-278-258-5841	Sequence 5841, Ap
40	31.8	1.1	51	65	US-60-213-360-2750	Sequence 2750, App	113	28.6	1.0	51	65	US-60-213-360-2838	Sequence 2838, Ap
41	31.6	1.1	51	76	US-60-324-185-3926	Sequence 3926, App	114	28.6	1.0	51	76	US-60-323-966-1090	Sequence 1090, App
42	31.4	1.1	51	76	US-60-324-185-4044	Sequence 4044, App	115	28.6	1.0	51	76	US-60-324-185-734	Sequence 734, App
43	31	1.1	60	34	US-09-908-975A-6403	Sequence 6403, App	116	28.6	1.0	51	76	US-60-324-185-4292	Sequence 4292, App
44	31	1.1	60	72	US-60-287-724-6403	Sequence 6403, App	117	28.6	1.0	60	34	US-09-908-975-7153	Sequence 7153, App
45	31	1.1	60	72	US-60-324-185-731	Sequence 731, App	118	28.6	1.0	60	34	US-09-908-975A-20382	Sequence 20382, A
46	30.8	1.1	51	36	US-09-953-188-448	Sequence 448, App	119	28.6	1.0	60	34	US-09-908-975A-7153	Sequence 7153, App
47	30.6	1.1	51	65	US-60-213-360-740	Sequence 740, App	120	28.6	1.0	60	34	US-09-908-975A-20382	Sequence 20382, A
48	30.6	1.1	51	65	US-60-250-830-971	Sequence 971, App	121	28.6	1.0	60	34	US-09-908-975A-20382	Sequence 20382, A
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50	30.6	1.1	51	60	US-09-908-975-6865	Sequence 6865, App	123	28.6	1.0	51	65	US-60-213-360-2762	Sequence 2762, App
51	30.6	1.1	60	34	US-09-908-975A-6865	Sequence 6865, App	124	28.2	1.0	51	71	US-60-278-258-1029	Sequence 1029, App
52	30.6	1.1	60	34	US-60-287-724-6865	Sequence 6865, App	125	28.2	1.0	51	76	US-60-324-185-1060	Sequence 1060, App
53	30.6	1.1	60	72	US-60-172-360-29095	Sequence 29095, A	126	28.2	1.0	51	76	US-60-324-185-1060	Sequence 1060, App
54	30.4	1.1	51	61	US-60-172-373-17815	Sequence 17815, A	127	28	1.0	51	29	US-09-755-374A-14111	Sequence 14111, A
55	30.4	1.1	51	61	US-60-213-359-338	Sequence 338, App	128	27.8	1.0	51	29	US-09-726-173A-6394	Sequence 6394, App
56	30.4	1.1	51	65	US-60-213-360-742	Sequence 742, App	129	27.8	1.0	51	29	US-09-755-374A-24991	Sequence 24991, A
57	30.4	1.1	51	65	US-60-213-360-749	Sequence 749, App	130	27.8	1.0	51	61	US-60-172-373-5424	Sequence 5424, App
58	30.4	1.1	51	65	US-60-250-830-986	Sequence 986, App	131	27.8	1.0	51	65	US-60-213-360-2841	Sequence 2841, App
59	30.4	1.1	51	65	US-60-250-830-986	Sequence 986, App	132	27.8	1.0	51	65	US-60-250-830-972	Sequence 972, App
60	30.4	1.1	51	71	US-60-278-258-5828	Sequence 5828, App	133	27.8	1.0	51	69	US-60-278-258-5787	Sequence 5787, App
61	30.4	1.1	51	76	US-60-324-185-3616	Sequence 3616, App	134	27.8	1.0	51	76	US-60-323-966-972	Sequence 972, App
62	30.4	1.1	51	76	US-60-324-185-3616	Sequence 3616, App	135	27.8	1.0	51	76	US-60-324-185-4108	Sequence 4108, App
63	30.4	1.1	51	76	US-60-324-185-4130	Sequence 4130, App	136	27.8	1.0	51	76	US-60-324-185-10481	Sequence 10481, A
64	30.4	1.1	51	76	US-60-324-185-4495	Sequence 4495, App	137	27.8	1.0	55	30	US-09-783-606-2380	Sequence 2380, App
65	30.2	1.1	51	65	US-60-213-360-2722	Sequence 2722, App	138	27.8	1.0	55	30	US-09-783-606-2380	Sequence 2380, App
66	30.2	1.1	51	65	US-60-213-360-2722	Sequence 2722, App	139	27.6	1.0	51	29	US-09-726-173A-5034	Sequence 5034, App
67	30.2	1.1	51	65	US-60-213-360-2763	Sequence 2763, App	140	27.6	1.0	51	65	US-60-213-360-2952	Sequence 2952, App
68	30.2	1.1	51	65	US-60-213-360-2946	Sequence 2946, App	141	27.6	1.0	51	69	US-60-250-830-943	Sequence 943, App
69	30.2	1.1	51	69	US-60-250-830-983	Sequence 983, App	142	27.6	1.0	51	76	US-60-323-966-943	Sequence 943, App
70	30.2	1.1	51	71	US-60-278-232-1483	Sequence 1483, App	143	27.6	1.0	51	76	US-60-324-185-3747	Sequence 3747, App
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72	30.2	1.1	51	71	US-60-278-258-5858	Sequence 5858, App	145	27.4	1.0	51	76	US-60-324-185-4281	Sequence 4281, App
73	30.2	1.1	51	71	US-60-278-561-12668	Sequence 12668, A	146	27.2	1.0	51	65	US-60-213-359-2530	Sequence 2530, App
74	30.2	1.1	51	76	US-60-324-185-4105	Sequence 4105, App	147	27.2	1.0	51	65	US-60-213-360-2952	Sequence 2952, App
75	30.2	1.1	51	76	US-60-324-185-4560	Sequence 4560, App	148	27.2	1.0	51	65	US-60-213-360-2952	Sequence 2952, App
76	30.2	1.1	51	76	US-60-324-185-4878	Sequence 4878, App	149	27.2	1.0	51	76	US-60-324-185-4586	Sequence 4586, App
77	30.2	1.1	51	76	US-60-324-185-4565	Sequence 4565, A	150	27.2	1.0	51	61	US-60-172-373-5314	Sequence 5314, App
78	30	1.1	51	65	US-60-213-359-336	Sequence 336, App	151	27	1.0	51	61	US-60-172-373-5314	Sequence 5314, App
79	30	1.1	51	65	US-60-213-359-339	Sequence 339, App	152	27	1.0	51	65	US-60-213-359-321	Sequence 321, App
80	30	1.1	51	69	US-60-250-830-974	Sequence 974, App	153	27	1.0	51	65	US-60-213-360-2999	Sequence 2999, App
81	30	1.1	51	69	US-60-250-830-987	Sequence 987, App	154	27	1.0	51	65	US-60-213-360-2999	Sequence 2999, App
82	30	1.1	51	76	US-60-323-966-974	Sequence 974, App	155	27	1.0	51	69	US-60-250-830-915	Sequence 915, App
83	30	1.1	51	76	US-60-323-966-987	Sequence 987, App	156	27	1.0	51	69	US-60-250-830-915	Sequence 915, App
84	30	1.1	51	76	US-60-324-185-3754	Sequence 3754, App	157	27	1.0	51	71	US-60-278-258-5849	Sequence 5849, App
85	30	1.1	55	62	US-60-184-841-2410	Sequence 2410, App	158	27	1.0	51	71	US-60-278-258-5849	Sequence 5849, App
86	29.8	1.1	51	65	US-60-213-360-2935	Sequence 2935, App	159	27	1.0	51	71	US-60-278-258-5849	Sequence 5849, App
87	29.8	1.1	51	65	US-60-213-360-2954	Sequence 2954, App	160	27	1.0	51	71	US-60-278-258-5849	Sequence 5849, App
88	29.8	1.1	51	65	US-60-250-830-949	Sequence 949, App	161	27	1.0	51	76	US-60-323-966-915	Sequence 915, App
89	29.8	1.1	51	76	US-60-323-966-949	Sequence 949, App	162	27	1.0	51	76	US-60-323-966-915	Sequence 915, App
90	29.8	1.1	51	76	US-60-324-185-4588	Sequence 4588, App	163	27	1.0	60	39	US-10-057-408-36	Sequence 36, App1
91	29.8	1.1	51	76	US-60-324-185-33831	Sequence 33831, A	164	26.8	1.0	51	61	US-60-172-373-5617	Sequence 5617, App
92	29.6	1.1	60	34	US-09-908-975-6992	Sequence 6992, App	165	26.8	1.0	51	65	US-60-213-359-335	Sequence 335, App
93	29.6	1.1	60	34	US-09-908-975A-6992	Sequence 6992, App	166	26.8	1.0	51	65	US-60-213-360-2967	Sequence 2967, App
94	29.6	1.1	60	72	US-60-287-724-6992	Sequence 6992, App	167	26.8	1.0	51	69	US-60-250-830-985	Sequence 985, App

168	26.8	1.0	51	76	US-60-323-966-985	Sequence 985, App	241	25.2	0.9	50	40	US-10-131-831-2511	Sequence 2511, App
C 169	26.6	1.0	51	29	US-09-755-374A-27828	Sequence 27828, A	242	25.2	0.9	50	40	US-10-131-831-2511	Sequence 3660, App
170	26.6	1.0	51	65	US-60-213-360-2978	Sequence 2978, App	243	25.2	0.9	51	65	US-60-213-360-2978	Sequence 2804, App
171	26.6	1.0	51	65	US-60-213-360-3103	Sequence 3103, App	244	25.2	0.9	51	69	US-60-250-830-953	Sequence 933, App
172	26.6	1.0	51	71	US-60-278-258-5831	Sequence 5831, App	245	25.2	0.9	51	71	US-60-278-258-5831	Sequence 5833, App
173	26.6	1.0	51	76	US-60-324-185-4152	Sequence 4152, App	246	25.2	0.9	51	76	US-60-324-185-4152	Sequence 933, App
174	26.6	1.0	51	76	US-60-324-185-4152	Sequence 3167, A	247	25.2	0.9	51	76	US-60-324-185-4152	Sequence 4109, App
175	26.6	1.0	56	39	US-10-057-408-49	Sequence 49, App1	248	25.2	0.9	60	34	US-09-908-975-6302	Sequence 6302, App
C 176	26.4	1.0	51	29	US-09-755-374A-14112	Sequence 14112, A	249	25.2	0.9	60	34	US-09-908-975-6302	Sequence 18186, A
177	26.4	1.0	51	76	US-60-324-185-4165	Sequence 4165, App	250	25.2	0.9	60	34	US-09-908-975A-6302	Sequence 6302, App
178	26.2	0.9	51	29	US-09-726-173A-6393	Sequence 6393, App	251	25.2	0.9	60	34	US-09-908-975A-6302	Sequence 18186, A
C 179	26.2	0.9	51	29	US-09-755-374A-24992	Sequence 24992, A	252	25.2	0.9	60	72	US-60-287-724-6302	Sequence 6302, App
180	26.2	0.9	51	65	US-60-213-360-2984	Sequence 2984, App	253	25.2	0.9	60	72	US-60-287-724-6302	Sequence 18186, A
181	26.2	0.9	51	69	US-60-250-830-1026	Sequence 1026, App	254	25.2	0.9	25	1	PCT-US02-21090-6	Sequence 6, App1
182	26.2	0.9	51	69	US-60-250-830-1026	Sequence 1026, App	255	25.2	0.9	25	33	US-09-898-556a-6	Sequence 6, App1
183	26.2	0.9	51	76	US-60-323-966-1026	Sequence 1026, App	256	25.2	0.9	51	61	US-60-172-373-17881	Sequence 17881, A
184	26.2	0.9	51	76	US-60-323-966-1026	Sequence 1026, App	257	25.2	0.9	51	61	US-60-213-360-2804	Sequence 2804, App
C 185	26	0.9	51	29	US-09-726-173A-5033	Sequence 5033, App	258	25.2	0.9	51	65	US-60-213-360-2876	Sequence 2876, App
C 186	26	0.9	51	29	US-09-755-374A-14114	Sequence 14114, A	259	25.2	0.9	51	65	US-60-213-360-2947	Sequence 2947, App
187	26	0.9	51	29	US-09-755-374A-24433	Sequence 24433, A	260	25.2	0.9	51	65	US-60-213-360-2953	Sequence 2953, App
188	26	0.9	51	29	US-09-755-374A-24434	Sequence 24434, A	261	25.2	0.9	51	65	US-60-213-360-3133	Sequence 3133, App
189	26	0.9	51	61	US-60-172-360-29463	Sequence 29463, A	262	25.2	0.9	51	65	US-60-213-360-3179	Sequence 3179, App
190	26	0.9	51	65	US-60-213-360-2802	Sequence 2802, App	263	25.2	0.9	51	69	US-60-250-830-1080	Sequence 1080, App
191	26	0.9	51	76	US-60-324-185-3925	Sequence 3925, App	264	25.2	0.9	51	71	US-60-278-258-5756	Sequence 5756, App
C 192	25.8	0.9	51	29	US-09-755-374A-14107	Sequence 14107, A	265	25.2	0.9	51	71	US-60-278-258-5803	Sequence 5803, App
193	25.8	0.9	51	65	US-60-213-359-420	Sequence 420, App	266	25.2	0.9	51	76	US-60-323-966-1080	Sequence 1080, App
C 194	25.8	0.9	51	65	US-60-213-360-2755	Sequence 2755, App	267	25.2	0.9	51	76	US-60-324-185-4179	Sequence 4179, App
195	25.8	0.9	51	76	US-60-278-258-5870	Sequence 5870, App	268	25.2	0.9	51	76	US-60-324-185-4561	Sequence 4561, App
196	25.8	0.9	51	71	US-60-324-185-3953	Sequence 3953, App	269	25.2	0.9	51	76	US-60-324-185-4587	Sequence 4587, App
197	25.8	0.9	51	76	US-60-324-185-4104	Sequence 4104, App	270	25.2	0.9	51	76	US-60-324-185-4587	Sequence 35803, A
198	25.8	0.9	51	76	US-60-324-185-4178	Sequence 4178, App	271	24.8	0.9	51	71	US-60-278-258-5590	Sequence 3590, App
199	25.8	0.9	60	39	US-10-057-408-45	Sequence 45, App1	272	24.8	0.9	51	71	US-60-278-258-5843	Sequence 5843, App
200	25.6	0.9	51	65	US-60-213-359-311	Sequence 311, App	273	24.8	0.9	51	71	US-60-278-258-5843	Sequence 5843, App
201	25.6	0.9	51	65	US-60-213-360-2766	Sequence 2766, App	274	24.8	0.9	60	34	US-09-908-975-6660	Sequence 6660, App
202	25.6	0.9	51	65	US-60-213-360-2822	Sequence 2822, App	275	24.8	0.9	60	34	US-09-908-975-6664	Sequence 6664, App
203	25.6	0.9	51	69	US-60-250-830-956	Sequence 956, App	276	24.8	0.9	60	34	US-09-908-975-6664	Sequence 6659, App
204	25.6	0.9	51	69	US-60-250-830-1022	Sequence 1022, App	277	24.8	0.9	60	34	US-09-908-975A-6660	Sequence 6660, App
205	25.6	0.9	51	69	US-60-250-830-1048	Sequence 1048, App	278	24.8	0.9	60	34	US-09-908-975A-6664	Sequence 6664, App
206	25.6	0.9	51	71	US-60-278-258-5767	Sequence 5767, App	279	24.8	0.9	60	34	US-09-908-975A-6859	Sequence 6859, App
207	25.6	0.9	51	71	US-60-278-258-5781	Sequence 5781, App	280	24.8	0.9	60	72	US-60-287-724-6660	Sequence 6660, App
208	25.6	0.9	51	71	US-60-278-258-5797	Sequence 5797, App	281	24.8	0.9	60	72	US-60-287-724-6664	Sequence 6664, App
209	25.6	0.9	51	71	US-60-278-258-6273	Sequence 6273, App	282	24.8	0.9	60	72	US-60-287-724-6859	Sequence 6859, App
210	25.6	0.9	51	76	US-60-323-966-956	Sequence 956, App	283	24.6	0.9	51	29	US-09-755-374A-27475	Sequence 27475, A
211	25.6	0.9	51	76	US-60-323-966-1022	Sequence 1022, App	284	24.6	0.9	51	29	US-09-755-374A-27476	Sequence 27476, A
212	25.6	0.9	51	76	US-60-323-966-1048	Sequence 1048, App	285	24.6	0.9	51	61	US-60-172-373-17848	Sequence 17848, A
213	25.6	0.9	51	76	US-60-324-185-3608	Sequence 3608, App	286	24.6	0.9	51	61	US-60-172-373-17973	Sequence 17973, A
214	25.6	0.9	51	76	US-60-324-185-3787	Sequence 3787, App	287	24.6	0.9	51	65	US-60-213-359-418	Sequence 418, App
215	25.6	0.9	51	76	US-60-324-185-4544	Sequence 4544, App	288	24.6	0.9	51	65	US-60-213-360-2910	Sequence 2910, App
216	25.6	0.9	51	76	US-60-324-185-11021	Sequence 11021, A	289	24.6	0.9	51	69	US-60-250-830-1032	Sequence 1032, App
217	25.6	0.9	51	76	US-60-324-185-32332	Sequence 32332, A	290	24.6	0.9	51	71	US-60-278-232-8634	Sequence 8634, App
218	25.6	0.9	56	39	US-10-057-408-40	Sequence 40, App1	291	24.6	0.9	51	76	US-60-323-966-1032	Sequence 1032, App
219	25.6	0.9	60	34	US-09-908-975-6829	Sequence 6829, App	292	24.6	0.9	51	76	US-60-324-185-4102	Sequence 4102, App
220	25.6	0.9	60	34	US-09-908-975A-6829	Sequence 6829, App	293	24.6	0.9	51	76	US-60-324-185-4258	Sequence 4258, App
221	25.6	0.9	60	72	US-60-287-724-6829	Sequence 6829, App	294	24.6	0.9	51	76	US-60-324-185-4518	Sequence 4518, App
222	25.4	0.9	51	61	US-60-172-373-5407	Sequence 5407, App	295	24.6	0.9	51	76	US-60-324-185-4518	Sequence 4518, App
223	25.4	0.9	51	61	US-60-172-373-17769	Sequence 17769, A	296	24.6	0.9	51	76	US-60-324-185-14693	Sequence 14693, A
224	25.4	0.9	51	65	US-60-213-360-2778	Sequence 2778, App	297	24.6	0.9	55	39	US-10-057-408-50	Sequence 50, App1
225	25.4	0.9	51	65	US-60-213-360-2825	Sequence 2825, App	298	24.6	0.9	60	34	US-09-908-975-6759	Sequence 6759, App
226	25.4	0.9	51	71	US-60-278-232-1474	Sequence 1474, App	299	24.6	0.9	60	34	US-09-908-975A-6759	Sequence 6759, App
227	25.4	0.9	51	71	US-60-278-258-5696	Sequence 5696, App	300	24.6	0.9	60	72	US-60-287-724-6759	Sequence 6759, App
228	25.4	0.9	51	71	US-60-278-258-5799	Sequence 5799, App	C 301	24.4	0.9	51	29	US-09-755-374A-14113	Sequence 14113, A
229	25.4	0.9	51	71	US-60-278-258-5824	Sequence 5824, App	C 302	24.4	0.9	51	61	US-60-172-373-17867	Sequence 17867, A
230	25.4	0.9	51	76	US-60-324-185-3937	Sequence 3937, App	C 303	24.4	0.9	51	65	US-60-213-359-356	Sequence 356, App
231	25.4	0.9	51	76	US-60-324-185-3977	Sequence 3977, App	304	24.4	0.9	51	71	US-60-278-258-5754	Sequence 5754, App
232	25.4	0.9	51	76	US-60-324-185-4251	Sequence 4251, App	305	24.4	0.9	51	71	US-60-278-258-5779	Sequence 5779, App
233	25.4	0.9	51	76	US-60-324-185-50763	Sequence 30763, A	306	24.4	0.9	51	76	US-60-324-185-5123	Sequence 4123, App
234	25.4	0.9	60	34	US-09-908-975-7136	Sequence 7136, App	307	24.4	0.9	51	76	US-60-324-185-4413	Sequence 4413, App
235	25.4	0.9	60	34	US-09-908-975A-7136	Sequence 7136, App	308	24.4	0.9	51	76	US-60-324-185-10998	Sequence 10998, A
236	25.4	0.9	60	72	US-60-287-724-7136	Sequence 7136, App	309	24.4	0.9	51	76	US-60-324-185-10985	Sequence 30845, A
237	25.2	0.9	50	1	PCT-US01-47856-2511	Sequence 2511, App	310	24.4	0.9	60	34	US-09-908-975-6321	Sequence 6321, App
238	25.2	0.9	50	1	PCT-US01-47856-3660	Sequence 3660, App	311	24.4	0.9	60	34	US-09-908-975-6790	Sequence 6790, App
239	25.2	0.9	50	40	US-10-131-827-2511	Sequence 2511, App	312	24.4	0.9	60	34	US-09-908-975A-6321	Sequence 6321, App
240	25.2	0.9	50	40	US-10-131-827-3660	Sequence 3660, App	313	24.4	0.9	60	34	US-09-908-975A-6790	Sequence 6790, App

314	24.4	0.9	60	72	US-60-287-724-6321	Sequence 6321, Ap	C 387	23.2	0.8	50	12	US-08-810-325-2558	Sequence 2558, Ap
315	24.4	0.9	60	72	US-60-287-724-6321	Sequence 6790, Ap	C 388	23.2	0.8	50	49	US-60-012-458-35	Sequence 35, App
316	24.2	0.9	51	61	US-60-172-373-5406	Sequence 5406, Ap	C 389	23.2	0.8	51	25	US-09-755-374A-249	Sequence 249, App
317	24.2	0.9	51	61	US-60-172-373-12209	Sequence 12209, A	C 390	23.2	0.8	51	29	US-09-755-374A-250	Sequence 250, App
318	24.2	0.9	51	71	US-60-278-232-1466	Sequence 1466, Ap	C 391	23.2	0.8	51	61	US-60-172-373-5568	Sequence 5568, Ap
319	24.2	0.9	51	71	US-60-278-258-15070	Sequence 15070, A	C 392	23.2	0.8	51	61	US-60-213-360-3095	Sequence 3095, Ap
320	24.2	0.9	51	76	US-60-324-185-3766	Sequence 3766, Ap	C 393	23.2	0.8	51	65	US-60-324-185-4101	Sequence 4101, Ap
321	24	0.9	51	29	US-09-755-374A-5299	Sequence 5299, Ap	C 394	23.2	0.8	60	34	US-09-908-975-6404	Sequence 6404, Ap
322	24	0.9	51	29	US-60-213-359-580	Sequence 580, App	C 395	23.2	0.8	60	34	US-09-908-975A-6404	Sequence 6404, Ap
323	24	0.9	51	65	US-60-213-360-8845	Sequence 8845, Ap	C 396	23.2	0.8	60	72	US-60-287-724-6404	Sequence 6404, Ap
324	24	0.9	51	69	US-60-250-830-1017	Sequence 1017, Ap	C 397	23	0.8	51	29	US-09-726-173A-2987	Sequence 2987, Ap
325	24	0.9	51	71	US-60-278-232-6547	Sequence 6547, Ap	C 398	23	0.8	51	29	US-09-755-374A-27917	Sequence 27917, A
326	24	0.9	51	76	US-60-323-966-1017	Sequence 1017, Ap	C 399	23	0.8	51	61	US-60-172-373-773	Sequence 773, App
327	24	0.9	51	76	US-60-324-185-4030	Sequence 4030, Ap	C 400	23	0.8	51	61	US-60-172-377-733	Sequence 733, App
328	24	0.9	51	76	US-60-324-185-11000	Sequence 11000, A	C 401	23	0.8	51	65	US-60-213-360-2937	Sequence 2937, Ap
329	24	0.9	51	76	US-60-324-185-14093	Sequence 14093, A	C 402	23	0.8	51	71	US-60-278-258-6698	Sequence 5698, Ap
C 330	24	0.9	58	30	US-09-775-049-14	Sequence 14, Appl	C 403	23	0.8	51	71	US-60-278-258-5763	Sequence 5763, Ap
C 331	23.8	0.9	51	29	US-09-726-173A-6713	Sequence 6713, Ap	C 404	23	0.8	51	71	US-60-278-258-5879	Sequence 5879, Ap
332	23.8	0.9	51	29	US-09-755-374A-24357	Sequence 24357, A	C 405	23	0.8	51	71	US-60-278-258-5879	Sequence 5879, Ap
333	23.8	0.9	51	29	US-09-755-374A-24358	Sequence 24358, A	C 406	23	0.8	51	76	US-60-324-185-3678	Sequence 3678, Ap
334	23.8	0.9	51	61	US-60-172-373-5343	Sequence 5343, Ap	C 407	23	0.8	51	76	US-09-912-293-732	Sequence 732, App
335	23.8	0.9	51	61	US-60-172-373-5652	Sequence 5652, Ap	C 408	23	0.8	59	24	US-09-628-860-9	Sequence 9, Appl
336	23.8	0.9	51	61	US-60-172-373-5675	Sequence 5675, Ap	C 409	23	0.8	60	34	US-09-906-393A-34	Sequence 34, Appl
337	23.8	0.9	51	61	US-60-172-373-17799	Sequence 17799, A	C 410	23	0.8	60	34	US-09-908-975-6323	Sequence 6323, Ap
338	23.8	0.9	51	65	US-60-213-360-3728	Sequence 3728, Ap	C 411	23	0.8	60	34	US-09-908-975A-6323	Sequence 6323, Ap
339	23.8	0.9	51	65	US-60-213-360-2748	Sequence 2748, Ap	C 412	23	0.8	60	72	US-60-287-724-6323	Sequence 6323, Ap
340	23.8	0.9	51	65	US-60-213-360-8824	Sequence 8824, Ap	C 413	22.8	0.8	51	61	US-60-172-373-24959	Sequence 24959, A
341	23.8	0.9	51	65	US-60-213-360-2848	Sequence 2848, Ap	C 414	22.8	0.8	51	65	US-60-213-359-90	Sequence 90, Appl
342	23.8	0.9	51	65	US-60-213-360-9921	Sequence 9921, Ap	C 415	22.8	0.8	51	65	US-60-213-362-3122	Sequence 3122, App
343	23.8	0.9	51	71	US-60-278-232-10275	Sequence 10275, A	C 416	22.8	0.8	51	65	US-60-213-362-5456	Sequence 5456, Ap
C 344	23.8	0.9	51	71	US-60-278-258-5783	Sequence 5783, Ap	C 417	22.8	0.8	51	65	US-60-278-258-5769	Sequence 5769, Ap
345	23.8	0.9	51	71	US-60-278-258-5814	Sequence 5814, Ap	C 418	22.8	0.8	51	76	US-60-324-185-3614	Sequence 3614, Ap
346	23.8	0.9	51	71	US-60-278-258-9216	Sequence 9216, Ap	C 419	22.8	0.8	51	76	US-60-324-185-1187	Sequence 1187, Ap
347	23.8	0.9	51	76	US-60-324-185-5672	Sequence 5672, Ap	C 420	22.8	0.8	51	76	US-60-324-185-1602	Sequence 1602, A
348	23.8	0.9	51	76	US-60-324-185-3949	Sequence 3949, Ap	C 421	22.8	0.8	51	76	US-60-324-185-14682	Sequence 14682, A
349	23.8	0.9	51	76	US-60-324-185-4125	Sequence 4125, Ap	C 422	22.8	0.8	51	76	US-60-324-185-14682	Sequence 14682, A
350	23.8	0.9	51	76	US-60-324-185-4250	Sequence 4250, Ap	C 423	22.8	0.8	51	76	US-60-324-185-31882	Sequence 31882, A
351	23.8	0.9	51	76	US-60-324-185-4255	Sequence 4255, Ap	C 424	22.8	0.8	60	20	US-09-535-897-16793	Sequence 16793, A
352	23.8	0.9	51	76	US-60-324-185-4371	Sequence 4371, Ap	C 425	22.8	0.8	60	34	US-09-908-975-16334	Sequence 16334, A
C 353	23.8	0.9	51	76	US-60-324-185-8933	Sequence 8933, Ap	C 426	22.8	0.8	60	34	US-09-908-975-23585	Sequence 23585, A
C 354	23.8	0.9	55	39	US-10-057-408-41	Sequence 41, Appl	C 427	22.8	0.8	60	34	US-09-908-975A-16334	Sequence 16334, A
C 355	23.8	0.9	60	34	US-09-908-975-6437	Sequence 6437, Ap	C 428	22.8	0.8	60	34	US-09-908-975A-23585	Sequence 23585, A
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357	23.8	0.9	60	34	US-09-908-975-15198	Sequence 15198, A	C 430	22.8	0.8	60	72	US-60-287-724-16334	Sequence 16334, A
358	23.8	0.9	60	34	US-09-908-975A-6437	Sequence 6437, Ap	C 431	22.6	0.8	51	65	US-60-213-360-23585	Sequence 23585, A
359	23.8	0.9	60	34	US-09-908-975A-6557	Sequence 6557, Ap	C 432	22.6	0.8	51	71	US-60-278-232-1030	Sequence 1030, Ap
360	23.8	0.9	60	34	US-09-908-975A-15198	Sequence 15198, A	C 433	22.6	0.8	51	71	US-60-278-232-8741	Sequence 8741, Ap
361	23.8	0.9	60	72	US-60-287-724-6437	Sequence 6437, Ap	C 434	22.6	0.8	51	76	US-60-324-185-3647	Sequence 3647, Ap
362	23.8	0.9	60	72	US-60-287-724-6557	Sequence 6557, Ap	C 435	22.6	0.8	60	34	US-09-908-975-6392	Sequence 6392, Ap
C 363	23.8	0.9	60	72	US-60-287-724-15198	Sequence 15198, A	C 436	22.6	0.8	60	34	US-09-908-975A-6392	Sequence 6392, Ap
C 364	23.6	0.9	51	61	US-60-172-360-10854	Sequence 10854, A	C 437	22.6	0.8	44	69	US-60-287-724-6392	Sequence 6392, Ap
365	23.6	0.9	51	65	US-60-213-359-2526	Sequence 2526, Ap	C 438	22.4	0.8	44	69	US-60-253-978-11078	Sequence 11078
366	23.6	0.9	51	65	US-60-213-360-2744	Sequence 2744, Ap	C 439	22.4	0.8	51	61	US-60-172-360-7702	Sequence 7702, A
367	23.6	0.9	51	65	US-60-213-360-2813	Sequence 2813, Ap	C 440	22.4	0.8	51	61	US-60-172-373-17873	Sequence 17873, A
368	23.6	0.9	51	71	US-60-278-258-5758	Sequence 5758, Ap	C 441	22.4	0.8	51	71	US-60-278-258-5695	Sequence 5695, Ap
369	23.6	0.9	51	71	US-60-278-258-5875	Sequence 5875, Ap	C 442	22.4	0.8	51	71	US-60-278-258-5839	Sequence 5839, Ap
370	23.6	0.9	51	76	US-60-324-185-3927	Sequence 3927, Ap	C 443	22.4	0.8	51	76	US-60-324-185-4257	Sequence 4257, Ap
371	23.6	0.9	51	76	US-60-324-185-4036	Sequence 4036, Ap	C 444	22.4	0.8	54	39	US-60-324-185-4898	Sequence 4898, Ap
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373	23.4	0.8	51	61	US-60-172-360-14666	Sequence 14666, A	C 446	22.4	0.8	54	39	US-10-055-713-24	Sequence 24, Appl
374	23.4	0.8	51	61	US-60-172-360-21384	Sequence 21384, A	C 447	22.4	0.8	60	34	US-09-908-975-16416	Sequence 16416, A
375	23.4	0.8	51	61	US-60-172-377-6853	Sequence 6853, Ap	C 448	22.4	0.8	60	34	US-09-908-975-16416	Sequence 16416, A
376	23.4	0.8	51	65	US-60-213-360-2818	Sequence 2818, Ap	C 449	22.4	0.8	60	34	US-10-057-408-39	Sequence 39, Appl
377	23.4	0.8	51	71	US-60-278-258-5874	Sequence 5874, Ap	C 450	22.4	0.8	60	39	US-10-057-408-48	Sequence 48, Appl
378	23.4	0.8	51	71	US-60-278-258-5887	Sequence 5887, Ap	C 451	22.4	0.8	60	39	US-60-287-724-16416	Sequence 16416, A
379	23.4	0.8	51	76	US-60-324-185-3663	Sequence 3663, Ap	C 452	22.4	0.8	60	72	US-60-287-724-16416	Sequence 16416, A
380	23.4	0.8	51	76	US-60-324-185-4230	Sequence 4230, Ap	C 453	22.2	0.8	31	34	US-09-912-263-182	Sequence 182, App
381	23.4	0.8	51	76	US-60-324-185-10995	Sequence 10995, A	C 454	22.2	0.8	47	65	US-60-216-745-3868	Sequence 3868, Ap
C 382	23.4	0.8	51	76	US-60-324-185-30557	Sequence 30557, A	C 455	22.2	0.8	50	15	US-09-114-053-1088	Sequence 1088, Ap
C 383	23.4	0.8	60	34	US-09-908-975-17236	Sequence 17236, A	C 456	22.2	0.8	50	18	US-09-420-691-4261	Sequence 4261, Ap
C 384	23.4	0.8	60	34	US-09-908-975A-17236	Sequence 17236, A	C 457	22.2	0.8	51	29	US-09-726-173A-6714	Sequence 6714, Ap
C 385	23.4	0.8	60	72	US-60-287-724-17236	Sequence 17236, A	C 458	22.2	0.8	51	61	US-60-172-360-29241	Sequence 29241, A
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460 22.2 0.8 51 61 US-60-172-377-10606 Sequence 10606, A
461 22.2 0.8 51 65 US-60-213-360-2725 Sequence 2725, Ap
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463 22.2 0.8 51 65 US-60-213-360-2790 Sequence 2790, Ap
464 22.2 0.8 51 65 US-60-213-360-2905 Sequence 2905, Ap
465 22.2 0.8 51 65 US-60-213-360-2912 Sequence 2912, Ap
466 22.2 0.8 51 65 US-60-213-360-2913 Sequence 2913, Ap
467 22.2 0.8 51 65 US-60-213-360-2958 Sequence 2958, Ap
468 22.2 0.8 51 69 US-60-250-830-816 Sequence 816, App
469 22.2 0.8 51 69 US-60-250-830-947 Sequence 947, App
470 22.2 0.8 51 69 US-60-250-830-1005 Sequence 1005, Ap
471 22.2 0.8 51 69 US-60-250-830-1006 Sequence 1006, Ap
472 22.2 0.8 51 69 US-60-250-830-1045 Sequence 1045, Ap
473 22.2 0.8 51 71 US-60-278-232-10137 Sequence 10137, A
474 22.2 0.8 51 71 US-60-278-258-5992 Sequence 5992, Ap
475 22.2 0.8 51 71 US-60-278-561-11075 Sequence 11075, A
476 22.2 0.8 51 76 US-60-323-966-816 Sequence 816, App
477 22.2 0.8 51 76 US-60-323-966-947 Sequence 947, App
478 22.2 0.8 51 76 US-60-323-966-1005 Sequence 1005, Ap
479 22.2 0.8 51 76 US-60-323-966-1006 Sequence 1006, Ap
480 22.2 0.8 51 76 US-60-323-966-1045 Sequence 1045, Ap
481 22.2 0.8 51 76 US-60-324-185-3617 Sequence 3617, Ap
482 22.2 0.8 51 76 US-60-324-185-14797 Sequence 14797, A
483 22.2 0.8 60 24 US-09-635-644-11062 Sequence 11062, A
484 22.2 0.8 60 34 US-09-908-975-5840 Sequence 5840, Ap
485 22.2 0.8 60 34 US-09-908-975-5877 Sequence 5877, Ap
486 22.2 0.8 60 34 US-09-908-975-6637 Sequence 6637, Ap
487 22.2 0.8 60 34 US-09-908-975-8235 Sequence 8235, Ap
488 22.2 0.8 60 34 US-09-908-975A-5840 Sequence 5840, Ap
489 22.2 0.8 60 34 US-09-908-975A-5877 Sequence 5877, Ap
490 22.2 0.8 60 34 US-09-908-975A-6637 Sequence 6637, Ap
491 22.2 0.8 60 34 US-09-908-975A-8235 Sequence 8235, Ap
492 22.2 0.8 60 72 US-60-287-724-5840 Sequence 5840, Ap
493 22.2 0.8 60 72 US-60-287-724-5877 Sequence 5877, Ap
494 22.2 0.8 60 72 US-60-287-724-6637 Sequence 6637, Ap
495 22.2 0.8 60 72 US-60-287-724-8235 Sequence 8235, Ap
496 22.2 0.8 60 69 US-60-253-654-25104 Sequence 25104, A
497 22.2 0.8 40 69 US-60-255-592-25104 Sequence 25104, A
498 22.2 0.8 51 29 US-09-755-374A-13101 Sequence 13101, A
499 22.2 0.8 51 61 US-60-172-360-2006 Sequence 2006, Ap
500 22.2 0.8 51 61 US-60-172-373-18177 Sequence 18177, A
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ALIGNMENTS

RESULT 1

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US-09-908-975-6782
; Sequence 6782, Application US/09908975
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908, 975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6782
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-6782
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Query Match

2.2%; Score 60; DB 34; Length 60;

Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCAGAGGTTTCGCGAGAGGCTTAACCTGTTTAGGCACAGAGGGCACACTCAGTGCTT 60
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RESULT 2

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US-09-908-975A-6782
; Sequence 6782, Application US/09908975A
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
; FILE REFERENCE: 36688-0006
; CURRENT APPLICATION NUMBER: US/09/908, 975A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6782
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975A-6782
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Query Match 2.2%; Score 60; DB 34; Length 60;

Best Local Similarity 100.0%; Pred. No. 3,4e-06;

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QY 1792 GCAGAGGTTTCGCGAGAGGCTTAACCTGTTTAGGCACAGAGGGCACACTCAGTGCTT 1851
      |||||||
DB 1 GCAGAGGTTTCGCGAGAGGCTTAACCTGTTTAGGCACAGAGGGCACACTCAGTGCTT 60
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RESULT 3

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US-60-287-724-6782
; Sequence 6782, Application US/60287724
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
; FILE REFERENCE: 36688-0004
; CURRENT APPLICATION NUMBER: US/60/287,724
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6782
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-287-724-6782
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Query Match 2.2%; Score 60; DB 72; Length 60;

Best Local Similarity 100.0%; Pred. No. 3,4e-06;

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QY 1792 GCAGAGGTTTCGCGAGAGGCTTAACCTGTTTAGGCACAGAGGGCACACTCAGTGCTT 1851
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DB 1 GCAGAGGTTTCGCGAGAGGCTTAACCTGTTTAGGCACAGAGGGCACACTCAGTGCTT 60
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RESULT 4

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; US-60-172-373-18031
; Sequence 18031, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 18031
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00003872
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 410, G->T
; US-60-172-373-18031
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Query Match

1.8%; Score 51; DB 61; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1629 GGCCTTACCCGGAATCAACCTGTACACGACGAGACACTCAGGG 1679
DB 1 GGCCTTACCCGGAATCAACCTGTACACGACGAGACACTCAGGG 51
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RESULT 5

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; US-60-172-373-18032
; Sequence 18032, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 18032
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00003873
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 757, T->C
; US-60-172-373-18032
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Query Match 1.8%; Score 51; DB 61; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1974 TCACACCTCATTAACACGACGAGACATTCAGAGAGAACCTTATT 2024
DB 1 TCACACCTCATTAACACGACGAGACATTCAGAGAGAACCTTATT 51
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RESULT 6

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; US-09-718-321A-465/C
; Sequence 465, Application US/09718321A
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/09/718,321A
; CURRENT FILING DATE: 2002-06-20
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 465
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43297259
; US-09-718-321A-465
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Query Match

1.8%; Score 49.4; DB 28; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;

Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1378 GCTTAGCAGAGACACACCTCATCAGACACTTAAGACACACAGAG 1428
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RESULT 7

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; US-09-718-321A-869/C
; Sequence 869, Application US/09718321A
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/09/718,321A
; CURRENT FILING DATE: 2002-06-20
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 869
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43297259
; US-09-718-321A-869
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Query Match 1.8%; Score 49.4; DB 28; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1362 AGGAGTGTCAGACAGGCTTTAGCCAGAGCTCAGACCTCATCAGACTTA 1412
DB 1 AGGAGTGTCAGACAGGCTTTAGCCAGAGCTCAGACCTCATCAGACTTA 1412
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Db 51 AGGAGTGTAGCAAGGCTTTAGCCGGAAGTCACACCTCATGACACTTA 1

RESULT 8

US-60-172-373-18033
; Sequence 18033, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 18033
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00024175
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 615, C->T
US-60-172-373-18033

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 61; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1334 GGGCAGACTCAGGTCCTTTGTGTGACAGGAGTGTGGCAGGCTTTGTG 1884
Db 1 GGGCAGACTCAGTGCCTTTGTGTGTAGGAGTGTGGCAGGCTTTGTG 51

RESULT 9

US-60-278-258-5294
; Sequence 5294, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5294
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00075163
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 421, T->G
US-60-278-258-5294

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 71; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AGGAGAAAGACTCCAGACTCCTGTTGGAGAGTAAGCAAAAATGGCACTT 693
Db 1 AGGAGAAAGACTCCAGACTCCTGTTGGAGAGTAAGCAAAAATGGCACTT 51

RESULT 10

US-60-278-258-5296
; Sequence 5296, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5296
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00075165
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 914, A->C
US-60-278-258-5296

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 71; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1136 GAAGTCAGACTCTTTACACATCAAGGAGACACACTCAAGGCTCAAGCCTTA 1186
Db 1 GAAGTCAGACTCTTTACACATCAAGGAGACACACTCAAGGCTCAAGCCTTA 51

RESULT 11

US-60-278-258-5297
; Sequence 5297, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5297
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00075166
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 2262, C->T
US-60-278-258-5297

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 71; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2483 TTGCTGTCTTTCTCCGATTTGATCCACCCCTTCACCTATTATTAAGTATA 2533
Db 1 TTGCTGTCTTTCTCCGATTTGATCTCAACCCCTTCACCTATTATTAAGTATA 51

```
RESULT 12
US-60-324-185-24475
; Sequence 24475, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 24475
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00115145
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 2091, C->G
US-60-324-185-24475

Query Match
Best Local Similarity 1.8%; Score 49.4; DB 76; Length 51;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2060 CACCTTATCAGACATCAGAGGACACACTCAGATAGAACTTTATGTGTA 2110
DB 1 CAACTTATCAGACATCAGAGGACACACTCAGATAGAACTTTATGTGTA 51

RESULT 13
US-50-278-258-5295
; Sequence 5295, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5295
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00075164
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 886, T->G
US-60-278-258-5295

Query Match
Best Local Similarity 1.7%; Score 47.8; DB 71; Length 51;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1108 GCAAGATTGTGAGCAGAGCTTACTTGAAGTGAACCTCTTACACATC 1158
DB 1 GCAAGATTGTGAGCAGAGCTTACTTGAAGTGAACCTCTTACACATC 51
```

```
RESULT 14
US-60-324-185-4221
; Sequence 4221, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4221
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00106336
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1082325.11, 1102, C->T
US-60-324-185-4221

Query Match
Best Local Similarity 1.5%; Score 41.4; DB 76; Length 51;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 994 GCACACACTCTGGGGAAAGCCTTATGTGTGTCAGAGGATGTGGCGAGCT 1044
DB 1 GGACACACTCAGGGGAAAGCCTTATGTGTGTCAGAGGATGTGGCGAGCT 51

RESULT 15
US-60-324-185-4223
; Sequence 4223, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4223
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00097881
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1082325.7, 179, T->C
US-60-324-185-4223

Query Match
Best Local Similarity 1.5%; Score 40.4; DB 76; Length 51;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 240 TTCACCCAGAGGAGGAGGCTTGTGAGCCCTGCTCAGAGGAGCCCTGCA 289
DB 2 TTCACCCAGAGGAGGAGGCTTGTGAGCCCTGCTCAGAGGAGCCCTGCTGTA 51

RESULT 16
```

```
US-60-213-359-20
; Sequence 20, Application US/60213359
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00082481
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 010741.4, 633, A->G
US-60-213-359-20
```

```
Query Match 1.4%; Score 39.8; DB 65; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.2;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy 224 GGATGTGCTGTGTTACTTACCCAGAGAGTGGAGTGTGTGAGCCCTGC 274
Db 1 GGATGTGCTGTGCTTCACCCAGAGAGTGAAGTATGTGATTCGC 51
```

```
RESULT 17
US-60-234-690-1769/c
; Sequence 1769, Application US/60234690
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0021 P
; CURRENT APPLICATION NUMBER: US/60/234,690
; CURRENT FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 12060
; SOFTWARE: PERL Program
; SEQ ID NO 1769
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00096187
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1005180.1, 448, G->A
US-60-234-690-1769
```

```
Query Match 1.4%; Score 38.2; DB 67; Length 51;
Best Local Similarity 84.3%; Pred. No. 6.4;
Matches 43; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 2464 TGAGAACTGCTCTCCATTGGTGTGCTTCCTCCGATTGATCCCAACC 2514
Db 51 TGAGAACTGCTCTCCTGTTGGCAAGCTTCTCCTGATGTGATCCCAACC 1
```

```
RESULT 18
US-60-323-843-1769/c
```

```
; Sequence 1769, Application US/60323843
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0021-1 P
; CURRENT APPLICATION NUMBER: US/60/323,843
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 12060
; SOFTWARE: PERL Program
; SEQ ID NO 1769
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00096187
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1005180.1, 448, G->A
US-60-323-843-1769
```

```
Query Match 1.4%; Score 38.2; DB 76; Length 51;
Best Local Similarity 84.3%; Pred. No. 6.4;
Matches 43; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 2464 TGAGAACTGCTCTCCATTGGTGTGCTTCCTCCGATTGATCCCAACC 2514
Db 51 TGAGAACTGCTCTCCTGTTGGCAAGCTTCTCCTGATGTGATCCCAACC 1
```

```
RESULT 19
US-60-324-185-26975
; Sequence 26975, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 26975
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00114633
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 399311.5, 1432, C->G
US-60-324-185-26975
```

```
Query Match 1.3%; Score 35.6; DB 76; Length 51;
Best Local Similarity 82.0%; Pred. No. 36;
Matches 41; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
Qy 1080 ACACACTCAGGGGAGAACTTATGTGTGCAAGATTGTGACGAGGCTT 1129
Db 2 ACACACTCAGGGGAGAACTTGTGTGTAGAGATGTGGCAAGATT 51
```

```
RESULT 20
US-60-213-359-2531
; Sequence 2531, Application US/60213359
```



```
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the identification of sequence polymorphisms using
; TITLE OF INVENTION: Polynucleotide sequence databases, and single nucleotide polymor
; TITLE OF INVENTION: Identified thereby
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 2531
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP0077379
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 481631.7, 204, C->T
; US-60-213-359-2531
```

```
Query Match 1.3% Score 35; DB 65; Length 51;
Best Local Similarity 80.4%; Pred. No. 54;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Oy 278 GAGGACCCCTGCAGGAGGTGATGCTGTATACCATCGGCTC 328
Db 1 GAGGACTCTATACAGGAGCGATGTTGGAGATTATAGAACCTGGTCTC 51
```

```
RESULT 21
; US-09-908-975-6663
; Sequence 6663, Application US/09908975
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, AVI
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6663
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-908-975-6663
```

```
Query Match 1.3% Score 35; DB 34; Length 60;
Best Local Similarity 74.6%; Pred. No. 58;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

```
Oy 1041 GGCTTTAGTGAGTCAAACTGATCAGACATGAGGAGGAGGAGAAACC 1099
Db 1 GCCTTTCCAGAGTGCACCTCAGAGTACATCAGAGATGCACACAGGGGAGAAACC 59
```

```
RESULT 22
; US-09-908-975A-6663
; Sequence 6663, Application US/09908975A
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, AVI
```

```
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0006
; CURRENT APPLICATION NUMBER: US/09/908,975A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6663
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-908-975A-6663
```

```
Query Match 1.3% Score 35; DB 34; Length 60;
Best Local Similarity 74.6%; Pred. No. 58;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

```
Oy 1041 GGCTTTAGTGAGTCAAACTGATCAGACATGAGGAGGAGGAGAAACC 1099
Db 1 GCCTTTCCAGAGTGCACCTCAGAGTACATCAGAGATGCACACAGGGGAGAAACC 59
```

```
RESULT 23
; US-60-287-724-6663
; Sequence 6663, Application US/60287724
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, AVI
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0004
; CURRENT APPLICATION NUMBER: US/60/287,724
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6663
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-287-724-6663
```

```
Query Match 1.3% Score 35; DB 72; Length 60;
Best Local Similarity 74.6%; Pred. No. 58;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

```
Oy 1041 GGCTTTAGTGAGTCAAACTGATCAGACATGAGGAGGAGGAGAAACC 1099
Db 1 GCCTTTCCAGAGTGCACCTCAGAGTACATCAGAGATGCACACAGGGGAGAAACC 59
```

```
RESULT 24
; US-09-726-173A-4584
; Sequence 4584, Application US/09726173A
; GENERAL INFORMATION:
; APPLICANT: Shinkels, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE ACID POLYMORPHISMS AND
; FILE REFERENCE: 15966-600
; CURRENT APPLICATION NUMBER: US/09/726,173A
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/168,138
```

```
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 7024
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 4584
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (26)..(0)
; OTHER INFORMATION: 2 of 2 allelic variants (4583 is other entry)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Accession number cg43960167
US-09-726-173A-4584

Query Match
Best Local Similarity 1.2%; Score 34.6; DB 29; Length 51;
Matches 40; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db
1 AGACAATGCTAGGCGAGATAGGGGTACCTGCTGAACCCACCT 2423
2375 AGTCAATGCCAGCAGATAGGGGTACCTGCTGAACCCACCT 2423
||||| ||||||| ||||||| ||| ||||||| |||
1 AGACAATGCTAGGCGAGATAGGGGTACCTGAACCCACCT 49

RESULT 25
US-60-324-185-4342
; Sequence 4342, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4342
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00121020
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1085739.1, 1554, A->G
US-60-324-185-4342

Query Match
Best Local Similarity 1.2%; Score 33.6; DB 76; Length 51;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db
1056 TCAACCGCATCAGACATCAGAGACACACTAGGGGGAACCTTAT 1103
||||| ||||||| ||||||| ||| ||||||| |||
3 TCAACCTTATCAGACATCAGAGATGAGGAGAACCTTAT 50

RESULT 26
US-60-172-360-29152
; Sequence 29152, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
```

```
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 29152
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00043257
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 430544.1, 203, T->G
US-60-172-360-29152

Query Match
Best Local Similarity 1.2%; Score 33.4; DB 61; Length 51;
Matches 37; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db
213 GTGCATTCAGGAGATGCGCTGTACTTCACCCAGAGAGT 255
9 GTGCCCTTGATGATGTGCTGTGAACCTCACCCAGAGAGT 51

RESULT 27
US-60-250-830-1043
; Sequence 1043, Application US/60250830
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0020 P
; CURRENT FILING DATE: 2000-11-04
; NUMBER OF SEQ ID NOS: 3246
; SOFTWARE: PERL Program
; SEQ ID NO 1043
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00121038
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1079415.2, 442, G->A
US-60-250-830-1043

Query Match
Best Local Similarity 1.2%; Score 33.4; DB 69; Length 51;
Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db
229 TGGCTGTACTTCACCCAGAGAGTGTGTTGACCCCTCTCAGA 279
||||| ||||||| ||||||| ||| ||| |||
1 TGGCTGTGACTTCACCCAGAGAGTGTGTTGACCTGATCAACTCAGA 51

RESULT 28
US-60-323-966-1043
; Sequence 1043, Application US/60323966
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0020-1 P
; CURRENT APPLICATION NUMBER: US/60/323,966
```



```
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5877
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00065280
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1090204.1, 730, A->G
US-60-278-258-5877

Query Match
Best Local Similarity 1.2%; Score 32.4; DB 71; Length 51;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1071 CATCAGAGACACTCAGGGAGAAACCTTATGTGTGCAAGATTGTGG 1120
    ||||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 1 CATCAGAGATATACACACTGTGTGAGACCCCTATGATGTAAAGAGTGTGG 50

RESULT 33
US-60-324-185-4224
; Sequence 4224, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4224
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00097882
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1082325.7, 1433, A->G
US-60-324-185-4224

Query Match
Best Local Similarity 1.2%; Score 32.4; DB 76; Length 51;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1239 CACGAGAGGGCGACACTGTGAGGAGACCTTATGTTTGGAGGAGATGTGG 1288
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 2 CACAGCGGACACACACTGTGGAGAGCCGCTATGTTGTGGGTGTGTGG 51

RESULT 34
US-60-324-185-6741
; Sequence 6741, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
```

```
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 6741
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00118792
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1142546.1, 616, G->A
US-60-324-185-6741

Query Match
Best Local Similarity 1.2%; Score 32.4; DB 76; Length 51;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1072 ATCAGAGACACACTCAGGGAGAAACCTTATGTGTGCAAGATTGTGGA 1121
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 1 ATATATAGAACACATACAGGGAGAAACCCCTATGATGTATGATGAATGTGA 50

RESULT 35
US-60-213-359-1622
; Sequence 1622, Application US/60213359
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 1622
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00089876
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 332474.3, 556, G->A
US-60-213-359-1622

Query Match
Best Local Similarity 1.2%; Score 32; DB 65; Length 51;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 276 CAGAGACCCCTGACACAGGAGGTGATGCTGAGACTTAAACCATCTG 323
    ||||| ||||| || ||| ||||| ||||| ||||| ||||| |||||
Db 3 CAGAGACCCCTGTACCAGAGTATATGCTGGAGAACTACAGCACCTG 50

RESULT 36
US-60-213-360-2926
; Sequence 2926, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
```

```
SOFTWARE: PERL Program
SEQ ID NO 2926
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00078765
LOCATION: 26
OTHER INFORMATION: 1085739.1, 1554, G->A
US-60-213-360-2926
```

```
Query Match
Best Local Similarity 79.2%; Score 32; DB 65; Length 51;
Pred. No. 4e+02; Mismatches 10; Indels 0; Gaps 0;
Matches 38; Conservative 0;
```

```
OY 1056 TCAAACCTGATCAGACATCAGAGACACATCAGGAGAAACCTTAT 1103
DB 3 TCAAACCTGATCAGACATCAGAGAAATTCATAGTGGGAGAACCTTAT 50
```

RESULT 37

```
US-60-230-830-822
Sequence 822, Application US/60250830
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
FILE REFERENCE: GX-0020 P
CURRENT APPLICATION NUMBER: US/60/250,830
NUMBER OF SEQ ID NOS: 3246
SOFTWARE: PERL Program
SEQ ID NO 822
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00104016
LOCATION: 26
OTHER INFORMATION: 332474.3, 558, G->A
US-60-250-830-822
```

```
Query Match
Best Local Similarity 79.2%; Score 32; DB 69; Length 51;
Pred. No. 4e+02; Mismatches 10; Indels 0; Gaps 0;
Matches 38; Conservative 0;
```

```
OY 276 CAGAGACCTGACAGGAGGTGCTGAGACCTTATACCATCTG 323
DB 3 CAGAGACCTGCTACAGAGATGTAATGCTGAGAACTACACCACTG 50
```

RESULT 38

```
US-60-323-966-822
Sequence 822, Application US/60323966
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
FILE REFERENCE: GX-0020-1 P
CURRENT APPLICATION NUMBER: US/60/323,966
NUMBER OF SEQ ID NOS: 3246
SOFTWARE: PERL Program
```

```
SEQ ID NO 822
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00104016
LOCATION: 26
OTHER INFORMATION: 332474.3, 558, G->A
US-60-323-966-822
```

```
Query Match
Best Local Similarity 79.2%; Score 32; DB 76; Length 51;
Pred. No. 4e+02; Mismatches 10; Indels 0; Gaps 0;
Matches 38; Conservative 0;
```

```
OY 276 CAGAGACCTGACAGGAGGTGCTGAGACCTTATACCATCTG 323
DB 3 CAGAGACCTGCTACAGAGATGTAATGCTGAGAACTACACCACTG 50
```

RESULT 39

```
US-60-172-373-5588
Sequence 5588, Application US/60172373
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
FILE REFERENCE: GX-0006 P
CURRENT APPLICATION NUMBER: US/60/172,373
NUMBER OF SEQ ID NOS: 25,772
SOFTWARE: PERL Program
SEQ ID NO 5588
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00024052
LOCATION: 26
OTHER INFORMATION: 482033.2, 1229, C->A
US-60-172-373-5588
```

```
Query Match
Best Local Similarity 76.5%; Score 31.8; DB 61; Length 51;
Pred. No. 4.5e+02; Mismatches 12; Indels 0; Gaps 0;
Matches 39; Conservative 0;
```

```
OY 1200 TGTGGCAGACCTTACCTGCAAGTCAACCTCTATACCCACGAGAGCG 1250
DB 1 TGTGGCCTGGGCTTCACGACGAGGTAAACCTCATCTCCACGAGAGCG 51
```

RESULT 40

```
US-60-213-360-2750/c
Sequence 2750, Application US/60213360
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
FILE REFERENCE: GX-0014 P
CURRENT APPLICATION NUMBER: US/60/213,360
NUMBER OF SEQ ID NOS: 8347
SOFTWARE: PERL Program
SEQ ID NO 2750
```

```

: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00088806
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1077932.1, 29, C->T
US-60-213-360-2750

Query Match
Best Local Similarity 1.1%; Score 31.8; DB 65; Length 51;
Pred. No. 4.5e+02;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1063 TGATCACACATCAGGACACATCAGGAGAAACCTATGTCGCAAG 1113
DB 51 TGATTGACATCAGCAGACTCACACAGGAGAAACCTATCAGTGAAG 1

RESULT 41
US-60-324-185-3926
: Sequence 3926, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324.185
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 3926
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00112420
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1076673.1, 794, A->G
US-60-324-185-3926

Query Match
Best Local Similarity 1.1%; Score 31.6; DB 76; Length 51;
Pred. No. 5.2e+02;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1251 CACACTGGGAGAGCCTTATGTTGCAGGAACTGG 1288
DB 5 CACACTGGTGAAGCCTTACCTATGAGTGAATGTGG 42

RESULT 42
US-60-324-185-4044
: Sequence 4044, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324.185
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 4044
: LENGTH: 51
```

```

: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00105120
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1079501.1, 272, G->A
US-60-324-185-4044

Query Match
Best Local Similarity 1.1%; Score 31.4; DB 76; Length 51;
Pred. No. 5.9e+02;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 214 TGGATTGAGGATGTGGCTGTACTCACCAGGAGAGAGTGG 262
DB 3 TGACCTTAAGAGATGTGGCTGTGATCTTCACTGAGAGAGAGCTGGGCT 51

RESULT 43
US-09-908-975-6403
: Sequence 6403, Application US/09908975
: GENERAL INFORMATION:
: APPLICANT: SHOSHAN, AVI
: APPLICANT: WASSERMAN, ALON
: APPLICANT: MINTZ, ELI
: APPLICANT: MINTZ, LIAT
: APPLICANT: FAIGLER, SIMCHON
: TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
: TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
: FILE REFERENCE: 36688-0005
: CURRENT APPLICATION NUMBER: US/09/908.975
: CURRENT FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: US 60/287,724
: PRIOR FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/221,607
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 32337
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 6403
: LENGTH: 60
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-908-975-6403

Query Match
Best Local Similarity 1.1%; Score 31; DB 34; Length 60;
Pred. No. 8.4e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1419 CACACAGGAGAGAACCTTATGTATGCACAGATGTGG 1457
DB 15 CACACAGGAGAGAACCTTATGTATGCACAGATGTGG 53

RESULT 44
US-09-908-975A-6403
: Sequence 6403, Application US/09908975A
: GENERAL INFORMATION:
: APPLICANT: SHOSHAN, AVI
: APPLICANT: WASSERMAN, ALON
: APPLICANT: MINTZ, ELI
: APPLICANT: MINTZ, LIAT
: APPLICANT: FAIGLER, SIMCHON
: TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
: TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
: FILE REFERENCE: 36688-0006
: CURRENT APPLICATION NUMBER: US/09/908.975A
: CURRENT FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: US 60/287,724
: PRIOR FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/221,607
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 32337
```

```
SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6403
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975A-6403
```

```
Query Match
Best Local Similarity 1.1%; Score 31; DB 34; Length 60;
Pred. No. 8.4e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1419 CACACAGAGAGAACCTTATGTATGCACAGATGTGGC 1457
Db 15 CACACAGAGAGAGAACCTTATGTATGCACAGATGTGGC 53
```

```
RESULT 45
US-60-287-724-6403
; Sequence 6403, Application US/60287724
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
```

```
; FILE REFERENCE: 36688-0004
; CURRENT APPLICATION NUMBER: US/60/287,724
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6403
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-287-724-6403
```

```
Query Match
Best Local Similarity 1.1%; Score 31; DB 72; Length 60;
Pred. No. 8.4e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1419 CACACAGAGAGAACCTTATGTATGCACAGATGTGGC 1457
Db 15 CACACAGAGAGAGAACCTTATGTATGCACAGATGTGGC 53
```

```
RESULT 46
US-60-324-185-731
; Sequence 731, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: MORRIS, MacDonald
; APPLICANT: Lai, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
```

```
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00120539
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 017463.1, 155, T->C
US-60-324-185-731
```

```
Query Match
Best Local Similarity 1.1%; Score 30.8; DB 76; Length 51;
Pred. No. 8.8e+02;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 219 TTCAGGATGTGGCTGTGACTTCACCCAGAGAGAGTGGAGTGTGGAG 268
Db 1 TTAGAGAGATGTGGCTGTGACTTCACCCAGAGAGAGTGGAGTGTGGAG 50
```

```
RESULT 47
US-09-953-198-448
```

```
; Sequence 448, Application US/09953198
; GENERAL INFORMATION:
; APPLICANT: COMPUGEN LTD
; TITLE OF INVENTION: DATA BASE OF SNP
; FILE REFERENCE: 1351253
; CURRENT APPLICATION NUMBER: US/09/953,198
; CURRENT FILING DATE: 2001-08-12
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 448
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-953-198-448
```

```
Query Match
Best Local Similarity 1.1%; Score 30.6; DB 36; Length 41;
Pred. No. 9e+02;
Matches 33; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 274 CTCAGAGAGACCTGCGACAGAGAGTGTGAGTGTGAGACTT 312
Db 1 CCCAGAGAGACCTGCGACAGAGAGTGTGAGTGTGAGACTT 39
```

```
RESULT 48
US-60-213-360-740
```

```
; Sequence 740, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: MORRIS, MacDonald
; APPLICANT: Lai, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 740
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00078224
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1077201.1, 925, T->C
US-60-213-360-740
```

```
Query Match
Best Local Similarity 1.1%; Score 30.6; DB 65; Length 51;
Pred. No. 1e+03;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1675 CAGGAGAGAGACCTTGTATGTGCTGAGTGTGAGAGGCTTTA 1719
Db 2 CTGGGAGAGAGACCTTGTATGTGCTGAGTGTGAGAGGCTTTCA 46
```

```
RESULT 49
```


US-60-250-830-971
: Sequence 971, Application US/60250830
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0020 P
: CURRENT APPLICATION NUMBER: US/60/250,830
: CURRENT FILING DATE: 2000-11-04
: NUMBER OF SEQ ID NOS: 3246
: SOFTWARE: PERL Program
: SEQ ID NO 971
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00120410
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1080820.1, 293, T->G
US-60-250-830-971

Query Match
1.1%: Score 30.6; DB 69; Length 51;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 235 TGTACTTCACCCAGAGAGAGTGTGAGCCCTGCTCAGA 279
|||
1 TGAAGTTCACCCAGAGAGAGTGTGAGCCCTGCTCAGA 45

Db

RESULT 50
US-60-323-966-971
: Sequence 971, Application US/60323966
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0020-1 P
: CURRENT APPLICATION NUMBER: US/60/323,966
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 3246
: SOFTWARE: PERL Program
: SEQ ID NO 971
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00120410
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1080820.1, 293, T->G
US-60-323-966-971

Query Match
1.1%: Score 30.6; DB 76; Length 51;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 235 TGTACTTCACCCAGAGAGAGTGTGAGCCCTGCTCAGA 279
|||
1 TGAAGTTCACCCAGAGAGAGTGTGAGCCCTGCTCAGA 45

Db

Search completed: June 4, 2003, 12:07:57
Job time : 6069 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 10:40:35 ; Search time 389 Seconds

(Without alignments)
9973.053 Million cell updates/sec

Title: US-09-898-556a-3

Perfect score: 2772

Sequence: 1 cagcgcgcttaagctgttg.....ttctaccatcctacacct 2772

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 544182

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	1.0	60	9	US-10-057-408-36 Sequence 36, Appl
2	26.6	1.0	56	9	US-10-057-408-49 Sequence 49, Appl
3	25.8	0.9	60	9	US-10-057-408-45 Sequence 45, Appl
4	25.6	0.9	56	9	US-10-057-408-40 Sequence 40, Appl
5	25	0.9	25	9	US-09-898-556a-6 Sequence 6, Appl
6	24.6	0.9	55	9	US-10-057-408-50 Sequence 50, Appl
7	24	0.9	58	9	US-09-775-049-14 Sequence 14, Appl
8	23.8	0.9	55	9	US-10-057-408-41 Sequence 41, Appl
9	23	0.8	60	9	US-09-906-393A-34 Sequence 34, Appl
10	22.4	0.8	54	9	US-10-055-713-24 Sequence 24, Appl
11	22.4	0.8	60	9	US-10-057-408-39 Sequence 39, Appl
12	22.4	0.8	60	9	US-10-057-408-48 Sequence 48, Appl
13	22.2	0.8	31	9	US-09-912-263-182 Sequence 182, Appl
14	21.4	0.8	60	9	US-09-906-393A-33 Sequence 33, Appl
15	21	0.8	21	9	US-09-898-556a-4 Sequence 4, Appl
16	21	0.8	31	10	US-09-801-274-1402 Sequence 1402, Ap
17	21	0.8	45	9	US-10-057-408-56 Sequence 56, Appl
18	21	0.8	59	9	US-10-066-960-236 Sequence 236, App
19	21	0.8	59	9	US-09-849-928-236 Sequence 236, App

20	20.6	0.7	52	9	US-10-066-960-244 Sequence 244, App
21	20.6	0.7	52	9	US-09-849-928-244 Sequence 240, Appl
22	20.2	0.7	50	9	US-09-950-442-40 Sequence 40, Appl
23	20	0.7	20	9	US-09-898-556a-12 Sequence 12, Appl
24	20	0.7	20	9	US-09-898-556a-13 Sequence 13, Appl
25	20	0.7	20	9	US-09-898-556a-14 Sequence 14, Appl
26	20	0.7	20	9	US-09-898-556a-15 Sequence 15, Appl
27	20	0.7	20	9	US-09-898-556a-16 Sequence 16, Appl
28	20	0.7	20	9	US-09-898-556a-17 Sequence 17, Appl
29	20	0.7	20	9	US-09-898-556a-18 Sequence 18, Appl
30	20	0.7	20	9	US-09-898-556a-19 Sequence 19, Appl
31	20	0.7	20	9	US-09-898-556a-20 Sequence 20, Appl
32	20	0.7	20	9	US-09-898-556a-21 Sequence 21, Appl
33	20	0.7	20	9	US-09-898-556a-22 Sequence 22, Appl
34	20	0.7	20	9	US-09-898-556a-23 Sequence 23, Appl
35	20	0.7	20	9	US-09-898-556a-24 Sequence 24, Appl
36	20	0.7	20	9	US-09-898-556a-25 Sequence 25, Appl
37	20	0.7	20	9	US-09-898-556a-26 Sequence 26, Appl
38	20	0.7	20	9	US-09-898-556a-27 Sequence 27, Appl
39	20	0.7	20	9	US-09-898-556a-28 Sequence 28, Appl
40	20	0.7	20	9	US-09-898-556a-29 Sequence 29, Appl
41	20	0.7	20	9	US-09-898-556a-30 Sequence 30, Appl
42	20	0.7	20	9	US-09-898-556a-31 Sequence 31, Appl
43	20	0.7	20	9	US-09-898-556a-32 Sequence 32, Appl
44	20	0.7	20	9	US-09-898-556a-33 Sequence 33, Appl
45	20	0.7	20	9	US-09-898-556a-34 Sequence 34, Appl
46	20	0.7	20	9	US-09-898-556a-35 Sequence 35, Appl
47	20	0.7	20	9	US-09-898-556a-36 Sequence 36, Appl
48	20	0.7	20	9	US-09-898-556a-37 Sequence 37, Appl
49	20	0.7	20	9	US-09-898-556a-38 Sequence 38, Appl
50	20	0.7	20	9	US-09-898-556a-39 Sequence 39, Appl
51	20	0.7	20	9	US-09-898-556a-40 Sequence 40, Appl
52	20	0.7	20	9	US-09-898-556a-41 Sequence 41, Appl
53	20	0.7	20	9	US-09-898-556a-42 Sequence 42, Appl
54	20	0.7	20	9	US-09-898-556a-43 Sequence 43, Appl
55	20	0.7	20	9	US-09-898-556a-44 Sequence 44, Appl
56	20	0.7	20	9	US-09-898-556a-45 Sequence 45, Appl
57	20	0.7	20	9	US-09-898-556a-46 Sequence 46, Appl
58	20	0.7	20	9	US-09-898-556a-47 Sequence 47, Appl
59	20	0.7	20	9	US-09-898-556a-48 Sequence 48, Appl
60	20	0.7	20	9	US-09-898-556a-49 Sequence 49, Appl
61	20	0.7	20	9	US-09-898-556a-50 Sequence 50, Appl
62	20	0.7	20	9	US-09-898-556a-51 Sequence 51, Appl
63	20	0.7	20	9	US-09-898-556a-52 Sequence 52, Appl
64	20	0.7	20	9	US-09-898-556a-53 Sequence 53, Appl
65	20	0.7	20	9	US-09-898-556a-54 Sequence 54, Appl
66	20	0.7	20	9	US-09-898-556a-55 Sequence 55, Appl
67	20	0.7	20	9	US-09-898-556a-56 Sequence 56, Appl
68	20	0.7	20	9	US-09-898-556a-57 Sequence 57, Appl
69	20	0.7	20	9	US-09-898-556a-58 Sequence 58, Appl
70	20	0.7	20	9	US-09-898-556a-59 Sequence 59, Appl
71	20	0.7	20	9	US-09-898-556a-60 Sequence 60, Appl
72	20	0.7	20	9	US-09-898-556a-61 Sequence 61, Appl
73	20	0.7	20	9	US-09-898-556a-62 Sequence 62, Appl
74	20	0.7	20	9	US-09-898-556a-63 Sequence 63, Appl
75	20	0.7	20	9	US-09-898-556a-64 Sequence 64, Appl
76	20	0.7	20	9	US-09-898-556a-65 Sequence 65, Appl
77	20	0.7	20	9	US-09-898-556a-66 Sequence 66, Appl
78	20	0.7	20	9	US-09-898-556a-67 Sequence 67, Appl
79	20	0.7	20	9	US-09-898-556a-68 Sequence 68, Appl
80	20	0.7	20	9	US-09-898-556a-69 Sequence 69, Appl
81	20	0.7	20	9	US-09-898-556a-70 Sequence 70, Appl
82	20	0.7	20	9	US-09-898-556a-71 Sequence 71, Appl
83	20	0.7	20	9	US-09-898-556a-72 Sequence 72, Appl
84	20	0.7	20	9	US-09-898-556a-73 Sequence 73, Appl
85	20	0.7	20	9	US-09-898-556a-74 Sequence 74, Appl
86	20	0.7	20	9	US-09-898-556a-75 Sequence 75, Appl
87	20	0.7	20	9	US-09-898-556a-76 Sequence 76, Appl
88	20	0.7	20	9	US-09-898-556a-77 Sequence 77, Appl
89	20	0.7	20	9	US-09-898-556a-78 Sequence 78, Appl
90	20	0.7	20	9	US-09-898-556a-79 Sequence 79, Appl
91	20	0.7	20	9	US-09-898-556a-80 Sequence 80, Appl
92	20	0.7	20	9	US-09-898-556a-81 Sequence 81, Appl

93	20	0.7	20	9	US-09-898-556a-89	Sequence 89, Appl	165	18.8	0.7	49	9	US-09-151-771-6	Sequence 6, Appl1
94	20	0.7	31	10	US-09-801-274-1404	Sequence 1404, Ap	C 167	18.8	0.7	51	10	US-09-808-335-45	Sequence 45, Appl
95	20	0.7	50	9	US-09-941-947a-54	Sequence 54, Appl1	C 168	18.6	0.7	25	10	US-09-866-108-14626	Sequence 14626, A
96	20	0.7	55	10	US-09-866-514-6	Sequence 6, Appl1	C 169	18.6	0.7	38	9	US-09-930-423-2600	Sequence 2600, Ap
97	19.8	0.7	28	10	US-09-851-129a-13	Sequence 13, Appl1	C 170	18.6	0.7	42	9	US-10-223-074-73	Sequence 70, Appl
98	19.8	0.7	48	9	US-09-877-478-5464	Sequence 47, Appl	C 171	18.6	0.7	46	10	US-09-738-841-21	Sequence 21, Appl
99	19.8	0.7	57	9	US-09-500-700-47	Sequence 47, Appl	C 172	18.6	0.7	50	9	US-09-754-066-15	Sequence 15, Appl
100	19.8	0.7	60	7	US-08-781-986a-1661	Sequence 1661, Ap	C 173	18.6	0.7	51	10	US-09-826-630-7	Sequence 7, Appl1
101	19.6	0.7	48	9	US-09-864-785-3163	Sequence 3163, Ap	C 174	18.6	0.7	51	10	US-09-826-630-8	Sequence 8, Appl1
102	19.4	0.7	45	9	US-10-057-408-54	Sequence 54, Appl	C 175	18.6	0.7	55	9	US-09-921-209-72	Sequence 72, Appl
103	19.4	0.7	48	9	US-09-848-754a-7934	Sequence 7934, Ap	C 176	18.4	0.7	56	7	US-08-781-986a-5140	Sequence 5140, Ap
104	19.4	0.7	49	9	US-09-156-323-6	Sequence 6, Appl1	C 177	18.4	0.7	31	9	US-09-931-325-166	Sequence 2508, Ap
105	19.4	0.7	50	9	US-09-943-007a-9	Sequence 9, Appl1	C 178	18.4	0.7	38	9	US-09-730-289a-2308	Sequence 5, Appl1
106	19.4	0.7	54	9	US-10-287-919-1217	Sequence 1217, Ap	C 179	18.4	0.7	45	9	US-10-209-952-5	Sequence 6616, Ap
107	19.2	0.7	25	10	US-09-866-108-14627	Sequence 14627, A	C 180	18.4	0.7	48	9	US-09-780-533a-6616	Sequence 9, Appl1
108	19.2	0.7	25	10	US-09-866-108-14628	Sequence 14628, A	C 181	18.4	0.7	59	10	US-09-877-804-9	Sequence 1803, Ap
109	19.2	0.7	48	9	US-09-877-478-5531	Sequence 5531, Ap	C 182	18.4	0.7	60	7	US-08-781-986a-1803	Sequence 2001, Ap
110	19.2	0.7	57	9	US-10-198-069-30	Sequence 30, Appl	C 183	18.4	0.7	60	9	US-09-920-941-2001	Sequence 19, Appl
111	19.2	0.7	59	9	US-09-991-262-53	Sequence 53, Appl	C 184	18.4	0.7	60	9	US-09-979-999-19	Sequence 2001, Ap
112	19	0.7	19	9	US-09-898-556a-5	Sequence 5, Appl1	C 185	18.4	0.7	60	9	US-10-017-754-2001	Sequence 14629, A
113	19	0.7	30	10	US-09-785-632a-80	Sequence 80, Appl	C 186	18.2	0.7	25	10	US-09-866-108-14629	Sequence 30, Appl
114	19	0.7	31	10	US-09-801-274-1405	Sequence 1405, Ap	C 187	18.2	0.7	34	10	US-09-730-857-30	Sequence 2, Appl1
115	19	0.7	46	9	US-10-199-330-13	Sequence 13, Appl	C 188	18.2	0.7	43	10	US-09-994-420-2	Sequence 6, Appl1
116	19	0.7	46	9	US-10-199-334-13	Sequence 43, Appl	C 189	18.2	0.7	43	12	US-10-082-032-2	Sequence 2, Appl1
117	19	0.7	48	9	US-09-905-291a-57	Sequence 57, Appl	C 190	18.2	0.7	45	10	US-09-760-008a-6	Sequence 239, App
118	19	0.7	50	9	US-09-902-853-57	Sequence 57, Appl	C 191	18.2	0.7	46	9	US-09-989-299a-239	Sequence 239, App
119	19	0.7	50	9	US-09-907-824-57	Sequence 57, Appl	C 192	18.2	0.7	46	9	US-09-989-733-239	Sequence 239, App
120	19	0.7	50	9	US-09-907-841-57	Sequence 57, Appl	C 193	18.2	0.7	46	9	US-09-990-444-239	Sequence 239, App
121	19	0.7	50	9	US-09-904-011-57	Sequence 57, Appl	C 194	18.2	0.7	46	9	US-09-989-436-239	Sequence 239, App
122	19	0.7	50	9	US-09-906-838-57	Sequence 57, Appl	C 195	18.2	0.7	46	9	US-09-991-181-239	Sequence 239, App
123	19	0.7	50	9	US-09-907-613-57	Sequence 57, Appl	C 196	18.2	0.7	46	9	US-09-993-663-239	Sequence 239, App
124	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 197	18.2	0.7	46	9	US-09-990-438-239	Sequence 239, App
125	19	0.7	50	9	US-09-906-700-57	Sequence 57, Appl	C 198	18.2	0.7	46	9	US-09-990-562-239	Sequence 239, App
126	19	0.7	50	9	US-09-902-903-57	Sequence 57, Appl	C 199	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
127	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 200	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
128	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 201	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
129	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 202	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
130	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 203	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
131	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 204	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
132	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 205	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
133	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 206	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
134	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 207	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
135	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 208	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
136	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 209	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
137	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 210	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
138	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 211	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
139	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 212	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
140	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 213	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
141	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 214	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
142	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 215	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
143	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 216	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
144	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 217	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
145	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 218	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
146	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 219	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
147	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 220	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
148	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 221	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
149	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 222	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
150	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 223	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
151	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 224	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
152	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 225	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
153	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 226	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
154	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 227	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
155	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 228	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
156	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 229	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
157	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 230	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
158	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 231	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
159	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 232	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
160	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 233	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
161	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 234	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
162	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 235	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
163	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 236	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
164	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl	C 237	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
165	18.8	0.7	40	9	US-10-057-558-47	Sequence 47, Appl	C 238	18.2	0.7	46	10	US-09-989-723-239	Sequence 239, App

C 239	18.2	0.7	46	10	US-09-989-727-239	Sequence 239, App	312	17.6	0.6	35	10	US-09-947-925a-9	Sequence 9, Appl1
C 240	18.2	0.7	46	10	US-09-989-731-239	Sequence 239, App	313	17.6	0.6	38	10	US-09-930-423-445	Sequence 2415, Ap
C 241	18.2	0.7	46	10	US-09-989-732-239	Sequence 239, App	314	17.6	0.6	38	10	US-09-842-552-42	Sequence 44, Appl
C 242	18.2	0.7	46	10	US-09-991-073-239	Sequence 239, App	315	17.6	0.6	39	10	US-09-264-468b-11	Sequence 11, Appl
C 243	18.2	0.7	46	10	US-09-990-442-239	Sequence 239, App	316	17.6	0.6	40	9	US-10-150-051-2	Sequence 2, Appl1
C 244	18.2	0.7	46	10	US-09-981-163-239	Sequence 239, App	317	17.6	0.6	42	9	US-10-168-050-9	Sequence 2, Appl1
C 245	18.2	0.7	46	10	US-09-993-604-239	Sequence 239, App	318	17.6	0.6	42	10	US-09-728-466-23	Sequence 23, Appl
C 246	18.2	0.7	46	10	US-09-990-456-239	Sequence 239, App	319	17.6	0.6	45	9	US-09-956-086-23	Sequence 23, Appl
C 247	18.2	0.7	46	10	US-09-989-721-239	Sequence 239, App	320	17.6	0.6	45	9	US-09-918-156-70	Sequence 23, Appl
C 248	18.2	0.7	48	9	US-10-066-960-194	Sequence 194, App	321	17.6	0.6	45	9	US-09-918-156-70	Sequence 23, Appl
C 249	18.2	0.7	48	9	US-10-138-838-68	Sequence 68, Appl	322	17.6	0.6	48	9	US-09-780-533a-5956	Sequence 5956, Ap
C 250	18.2	0.7	48	9	US-10-139-031-68	Sequence 68, Appl	323	17.6	0.6	48	9	US-09-877-478-5308	Sequence 5308, Ap
C 251	18.2	0.7	48	9	US-09-780-533a-5788	Sequence 5788, Ap	324	17.6	0.6	48	9	US-09-877-478-5791	Sequence 5791, Ap
C 252	18.2	0.7	48	9	US-09-849-928-194	Sequence 194, App	325	17.6	0.6	48	9	US-09-776-474-2677	Sequence 2677, Ap
C 253	18.2	0.7	48	9	US-09-877-478-5801	Sequence 5801, Ap	326	17.6	0.6	48	9	US-09-780-164-2572	Sequence 2572, Ap
C 254	18.2	0.7	48	9	US-09-877-478-5849	Sequence 5849, Ap	327	17.6	0.6	48	9	US-09-930-423-4516	Sequence 4516, Ap
C 255	18.2	0.7	48	9	US-10-138-905-68	Sequence 68, Appl	328	17.6	0.6	50	7	US-08-781-986a-2237	Sequence 2237, Ap
C 256	18.2	0.7	48	9	US-10-138-916-68	Sequence 68, Appl	329	17.6	0.6	50	10	US-09-742-693-9	Sequence 9, Appl1
C 257	18.2	0.7	48	9	US-09-976-800-68	Sequence 68, Appl	330	17.6	0.6	51	7	US-08-781-986a-2847	Sequence 2847, Ap
C 258	18.2	0.7	52	7	US-08-781-986a-1748	Sequence 1748, Ap	331	17.6	0.6	53	9	US-09-904-557-10	Sequence 10, Appl
C 259	18.2	0.7	53	9	US-10-085-056-37	Sequence 37, Appl	332	17.6	0.6	53	10	US-09-263-959-588	Sequence 588, App
C 260	18.2	0.7	54	9	US-10-055-713-25	Sequence 25, Appl	333	17.6	0.6	53	10	US-09-975-408-13	Sequence 13, Appl
C 261	18.2	0.7	58	7	US-08-781-986a-5156	Sequence 5156, Ap	334	17.6	0.6	53	12	US-10-075-579-13	Sequence 13, Appl
C 262	18.2	0.7	60	9	US-09-907-111-277	Sequence 277, App	335	17.6	0.6	55	7	US-08-781-986a-2677	Sequence 2677, Ap
C 263	18.2	0.7	60	9	US-09-741-744a-143	Sequence 143, App	336	17.6	0.6	57	9	US-09-927-121B-68	Sequence 68, Appl
C 264	18.2	0.6	26	9	US-09-915-043-42	Sequence 42, Appl	337	17.6	0.6	57	10	US-09-850-165-27	Sequence 27, Appl
C 265	18.2	0.6	26	9	US-09-828-062-30	Sequence 30, Appl	338	17.6	0.6	58	7	US-08-781-986a-2018	Sequence 2018, Ap
C 266	18.2	0.6	43	9	US-10-081-408-7	Sequence 7, Appl1	339	17.6	0.6	60	9	US-09-841-513-19	Sequence 19, Appl
C 267	18.2	0.6	45	9	US-10-057-408-42	Sequence 42, Appl	340	17.6	0.6	60	9	US-09-994-064-49	Sequence 49, Appl
C 268	18.2	0.6	46	9	US-10-076-631-4	Sequence 4, Appl1	341	17.6	0.6	60	9	US-10-057-408-46	Sequence 46, Appl
C 269	18.2	0.6	48	9	US-09-848-754a-8144	Sequence 8144, Ap	342	17.6	0.6	60	9	US-09-995-529-181	Sequence 181, App
C 270	18.2	0.6	48	9	US-09-848-754a-8449	Sequence 8449, Ap	343	17.4	0.6	31	10	US-09-801-274-1723	Sequence 1723, Ap
C 271	18.2	0.6	48	9	US-09-930-423-4188	Sequence 4188, Ap	344	17.4	0.6	36	9	US-10-056-414-516	Sequence 516, App
C 272	18.2	0.6	49	9	US-09-952-060-18	Sequence 18, Appl	345	17.4	0.6	36	10	US-09-375-924C-8	Sequence 8, Appl1
C 273	18.2	0.6	49	10	US-09-753-436-72	Sequence 72, Appl	346	17.4	0.6	37	9	US-10-287-919-738	Sequence 738, App
C 274	18.2	0.6	53	9	US-09-918-156-60	Sequence 60, Appl	347	17.4	0.6	38	9	US-09-877-478-3724	Sequence 3724, Ap
C 275	18.2	0.6	60	7	US-08-781-986a-3448	Sequence 3448, Ap	348	17.4	0.6	38	9	US-09-848-754a-5040	Sequence 5040, Ap
C 276	18.2	0.6	60	9	US-09-907-111-256	Sequence 256, App	349	17.4	0.6	38	9	US-09-776-474-1533	Sequence 1533, Ap
C 277	18.2	0.6	60	9	US-10-059-271-60	Sequence 60, App	350	17.4	0.6	39	9	US-10-129-709-5	Sequence 5, Appl1
C 278	18.2	0.6	60	9	US-09-888-413-26	Sequence 26, Appl	351	17.4	0.6	42	9	US-10-043-573-131	Sequence 131, App
C 279	17.8	0.6	31	9	US-09-912-263-503	Sequence 503, App	352	17.4	0.6	42	9	US-09-954-594A-8	Sequence 8, Appl1
C 280	17.8	0.6	31	10	US-09-801-274-1403	Sequence 1403, App	353	17.4	0.6	42	9	US-09-954-594A-8	Sequence 8, Appl1
C 281	17.8	0.6	38	9	US-09-930-423-2953	Sequence 2953, Ap	354	17.4	0.6	42	9	US-09-974-685-8	Sequence 8, Appl1
C 282	17.8	0.6	40	9	US-10-150-051-4	Sequence 4, Appl1	355	17.4	0.6	42	9	US-09-974-685-8	Sequence 8, Appl1
C 283	17.8	0.6	45	10	US-09-943-692-5	Sequence 5, Appl1	356	17.4	0.6	42	10	US-09-865-807-8	Sequence 8, Appl1
C 284	17.8	0.6	47	9	US-10-103-002-3	Sequence 3, Appl1	357	17.4	0.6	42	10	US-09-865-807-8	Sequence 8, Appl1
C 285	17.8	0.6	47	9	US-09-465-925-4	Sequence 4, Appl1	358	17.4	0.6	44	10	US-09-943-215-17	Sequence 17, Appl
C 286	17.8	0.6	47	9	US-10-269-229-9	Sequence 9, Appl1	359	17.4	0.6	47	9	US-09-966-782a-34	Sequence 34, Appl
C 287	17.8	0.6	47	10	US-09-909-496-9	Sequence 9, Appl1	360	17.4	0.6	48	9	US-09-848-754a-8071	Sequence 8071, Ap
C 288	17.8	0.6	48	9	US-09-780-533a-6395	Sequence 6395, Ap	361	17.4	0.6	48	9	US-09-848-754a-8944	Sequence 8944, Ap
C 289	17.8	0.6	48	9	US-09-877-478-5639	Sequence 5639, Ap	362	17.4	0.6	48	9	US-09-780-164-2347	Sequence 2347, Ap
C 290	17.8	0.6	49	9	US-10-199-330-14	Sequence 14, Appl	363	17.4	0.6	49	9	US-09-376-940-9	Sequence 9, Appl1
C 291	17.8	0.6	49	9	US-10-198-334-14	Sequence 14, Appl	364	17.4	0.6	49	9	US-10-287-919-347	Sequence 347, App
C 292	17.8	0.6	49	9	US-10-152-297-16	Sequence 16, Appl	365	17.4	0.6	51	10	US-09-969-002-43	Sequence 43, Appl
C 293	17.8	0.6	49	9	US-10-152-297-17	Sequence 17, Appl	366	17.4	0.6	51	10	US-09-969-002-51	Sequence 51, Appl
C 294	17.8	0.6	49	10	US-09-790-417-117	Sequence 117, App	367	17.4	0.6	52	7	US-08-781-986a-1855	Sequence 1855, Ap
C 295	17.8	0.6	49	10	US-09-790-417-118	Sequence 118, App	368	17.4	0.6	54	7	US-08-781-986a-84	Sequence 84, Appl
C 296	17.8	0.6	50	9	US-10-073-300-14	Sequence 14, Appl	369	17.4	0.6	54	10	US-09-785-632a-84	Sequence 84, Appl
C 297	17.8	0.6	50	9	US-10-073-300-15	Sequence 15, Appl	370	17.4	0.6	54	10	US-08-878-574-13496	Sequence 13496, A
C 298	17.8	0.6	51	10	US-09-859-104-4	Sequence 4, Appl1	371	17.4	0.6	54	10	US-09-825-012-31	Sequence 31, Appl
C 299	17.8	0.6	52	9	US-10-04-427-11	Sequence 11, Appl	372	17.4	0.6	55	10	US-09-969-617-11	Sequence 11, Appl
C 300	17.8	0.6	52	9	US-10-287-919-1219	Sequence 1219, Ap	373	17.4	0.6	57	10	US-09-922-261-147	Sequence 147, App
C 301	17.8	0.6	53	9	US-09-907-111-267	Sequence 267, App	374	17.4	0.6	57	10	US-09-850-165-33	Sequence 33, Appl
C 302	17.8	0.6	53	9	US-09-907-111-269	Sequence 269, App	375	17.4	0.6	58	9	US-10-024-494-18	Sequence 18, Appl
C 303	17.8	0.6	54	9	US-10-004-427-47	Sequence 47, Appl	376	17.4	0.6	59	9	US-10-068-137-9	Sequence 9, Appl1
C 304	17.8	0.6	54	9	US-10-041-414-31	Sequence 31, Appl	377	17.4	0.6	59	10	US-09-983-965-1793	Sequence 1793, Ap
C 305	17.8	0.6	54	9	US-10-233-996-29	Sequence 29, Appl	378	17.2	0.6	25	10	US-09-769-864-39	Sequence 39, Appl
C 306	17.8	0.6	59	10	US-09-878-574-1776	Sequence 1776, Ap	379	17.2	0.6	25	10	US-09-866-108-14630	Sequence 14630, A
C 307	17.8	0.6	60	9	US-10-057-408-37	Sequence 37, Appl	380	17.2	0.6	38	9	US-10-012-898-2	Sequence 2, Appl1
C 308	17.8	0.6	60	10	US-09-735-705-370	Sequence 370, App	381	17.2	0.6	38	9	US-10-012-898-6	Sequence 6, Appl1
C 309	17.8	0.6	60	10	US-09-850-716a-370	Sequence 370, App	382	17.2	0.6	38	9	US-09-776-474-2038	Sequence 2038, Ap
C 310	17.8	0.6	60	10	US-09-897-778-370	Sequence 370, App	383	17.2	0.6	39	10	US-09-263-959-166	Sequence 166, App
C 311	17.6	0.6	25	10	US-09-866-108-14625	Sequence 14625, A	384	17.2	0.6	41	10	US-09-473-872-45	Sequence 45, Appl

C 385	17.2	0.6	42	9	US-10-139-480-9	Sequence 9, Appl1
C 386	17.2	0.6	46	9	US-10-103-686-19	Sequence 19, Appl1
C 387	17.2	0.6	46	9	US-09-019-441-19	Sequence 19, Appl1
C 388	17.2	0.6	47	9	US-09-848-616-5	Sequence 5, Appl1
C 389	17.2	0.6	48	9	US-09-780-533A-5975	Sequence 5975, Ap
C 390	17.2	0.6	48	9	US-09-877-478-5252	Sequence 5252, Ap
C 391	17.2	0.6	48	9	US-09-877-478-5257	Sequence 5257, Ap
C 392	17.2	0.6	48	9	US-09-848-754A-7902	Sequence 7902, Ap
C 393	17.2	0.6	48	9	US-09-848-754A-8159	Sequence 8159, Ap
C 394	17.2	0.6	48	9	US-09-848-754A-8219	Sequence 8219, Ap
C 395	17.2	0.6	48	9	US-10-140-164-71	Sequence 71, Appl1
C 396	17.2	0.6	48	9	US-10-140-164-74	Sequence 74, Appl1
C 397	17.2	0.6	48	9	US-09-930-423-4492	Sequence 4492, Ap
C 398	17.2	0.6	48	10	US-09-753-436-67	Sequence 67, Appl1
C 399	17.2	0.6	50	9	US-10-066-583-1715	Sequence 1715, Ap
C 400	17.2	0.6	51	7	US-08-781-986A-5132	Sequence 5132, Ap
C 401	17.2	0.6	51	10	US-09-866-778A-38	Sequence 38, Appl1
C 402	17.2	0.6	52	9	US-10-060-036-2090	Sequence 2090, Ap
C 403	17.2	0.6	52	10	US-09-007-093-19	Sequence 19, Appl1
C 404	17.2	0.6	56	7	US-08-781-986A-1915	Sequence 1915, Ap
C 405	17.2	0.6	57	9	US-10-156-604-15	Sequence 15, Appl1
C 406	17.2	0.6	58	7	US-08-781-986A-2796	Sequence 2796, Ap
C 407	17.2	0.6	58	7	US-08-781-986A-4980	Sequence 4980, Ap
C 408	17.2	0.6	60	9	US-10-083-357-421	Sequence 421, Ap
C 409	17.2	0.6	60	9	US-10-037-282-115	Sequence 115, Appl1
C 410	17.2	0.6	60	9	US-09-888-413-11	Sequence 11, Appl1
C 411	17.2	0.6	60	9	US-09-895-529-321	Sequence 321, Ap
C 412	17.2	0.6	60	9	US-09-995-529-325	Sequence 325, Ap
C 413	17.2	0.6	60	9	US-09-995-529-326	Sequence 326, Ap
C 414	17.2	0.6	60	10	US-09-919-124-7	Sequence 7, Appl1
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C 419	17.2	0.6	25	10	US-09-801-274-1139	Sequence 1139, Ap
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C 421	17.2	0.6	33	9	US-09-943-123-4	Sequence 4, Appl1
C 422	17.2	0.6	35	9	US-10-287-919-736	Sequence 736, Ap
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C 424	17.2	0.6	38	9	US-09-923-327-53	Sequence 53, Appl1
C 425	17.2	0.6	36	10	US-09-737-626A-16	Sequence 16, Appl1
C 426	17.2	0.6	38	9	US-09-864-785-1195	Sequence 1195, Ap
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C 431	17.2	0.6	43	10	US-09-774-021-15	Sequence 15, Appl1
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C 433	17.2	0.6	44	9	US-09-875-082-86	Sequence 86, Appl1
C 434	17.2	0.6	45	9	US-09-853-526-239	Sequence 239, Ap
C 435	17.2	0.6	45	9	US-10-012-896-942	Sequence 942, Ap
C 436	17.2	0.6	45	9	US-09-895-793-942	Sequence 942, Ap
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C 438	17.2	0.6	45	9	US-09-895-793-942	Sequence 942, Ap
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C 440	17.2	0.6	45	10	US-09-780-669-942	Sequence 942, Ap
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C 447	17.2	0.6	48	9	US-09-877-478-5632	Sequence 5632, Ap
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C 449	17.2	0.6	48	9	US-10-146-835-23	Sequence 23, Appl1
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C 452	17.2	0.6	48	10	US-09-975-408-7	Sequence 7, Appl1
C 453	17.2	0.6	48	12	US-10-075-579-7	Sequence 7, Appl1
C 454	17.2	0.6	50	7	US-08-781-986A-2775	Sequence 2775, Ap
C 455	17.2	0.6	50	7	US-08-781-986A-5105	Sequence 5105, Ap
C 456	17.2	0.6	50	9	US-09-269-921-91	Sequence 91, Appl1
C 457	17.2	0.6	51	7	US-08-781-986A-2059	Sequence 2059, Ap

458	17	0.6	51	9	US-10-105-963-24	Sequence 24, Appl1
459	17	0.6	52	9	US-09-844-653-39	Sequence 29, Appl1
460	17	0.6	53	9	US-10-066-543-3092	Sequence 3092, Ap
461	17	0.6	54	9	US-10-091-135-19	Sequence 19, Appl1
462	17	0.6	54	10	US-09-858-349-4	Sequence 4, Appl1
463	17	0.6	55	9	US-10-051-841-11	Sequence 11, Appl1
464	17	0.6	55	12	US-10-051-841-11	Sequence 11, Appl1
465	17	0.6	56	9	US-10-084-298-8	Sequence 8, Appl1
466	17	0.6	58	9	US-09-796-692-9235	Sequence 9235, Ap
467	17	0.6	58	9	US-10-040-862-9235	Sequence 9235, Ap
468	17	0.6	58	9	US-10-125-648-10	Sequence 10, Appl1
469	17	0.6	59	9	US-09-362-286-27	Sequence 27, Appl1
470	17	0.6	59	9	US-09-362-286-32	Sequence 32, Appl1
471	17	0.6	59	12	US-10-013-737-11	Sequence 11, Appl1
472	17	0.6	60	9	US-09-954-692-26	Sequence 26, Appl1
473	17	0.6	60	9	US-09-995-529-183	Sequence 183, Ap
474	17	0.6	60	10	US-09-559-671A-26	Sequence 26, Appl1
475	17	0.6	25	9	US-10-046-722-11	Sequence 11, Appl1
476	16.8	0.6	25	12	US-10-125-635A-357	Sequence 357, Ap
477	16.8	0.6	28	9	US-09-938-864-357	Sequence 357, Ap
478	16.8	0.6	28	9	US-09-785-019-357	Sequence 357, Ap
479	16.8	0.6	28	9	US-10-002-603-357	Sequence 357, Ap
480	16.8	0.6	31	9	US-09-963-875-19	Sequence 19, Appl1
481	16.8	0.6	31	9	US-10-136-891-17	Sequence 17, Appl1
482	16.8	0.6	31	10	US-09-801-274-353	Sequence 19, Appl1
483	16.8	0.6	31	10	US-09-801-274-353	Sequence 19, Appl1
484	16.8	0.6	33	10	US-09-991-960-3	Sequence 3, Appl1
485	16.8	0.6	36	9	US-10-056-414-735	Sequence 735, Ap
486	16.8	0.6	37	10	US-09-156-110A-15	Sequence 15, Appl1
487	16.8	0.6	38	9	US-09-848-754A-3907	Sequence 3907, Ap
488	16.8	0.6	39	10	US-09-874-470-11	Sequence 11, Appl1
489	16.8	0.6	39	10	US-09-874-470-12	Sequence 12, Appl1
490	16.8	0.6	39	12	US-10-108-714-5	Sequence 11, Appl1
491	16.8	0.6	40	9	US-10-112-488-61	Sequence 61, Appl1
492	16.8	0.6	41	9	US-10-043-573-110	Sequence 110, Ap
493	16.8	0.6	42	9	US-09-997-931-28	Sequence 28, Appl1
494	16.8	0.6	42	10	US-09-765-272-353	Sequence 353, Ap
495	16.8	0.6	44	9	US-09-913-238-27	Sequence 27, Appl1
496	16.8	0.6	44	9	US-09-913-238-27	Sequence 27, Appl1
497	16.8	0.6	44	9	US-09-913-238-27	Sequence 27, Appl1
498	16.8	0.6	44	9	US-09-913-238-27	Sequence 27, Appl1
499	16.8	0.6	44	9	US-09-913-238-27	Sequence 27, Appl1
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ALIGNMENTS

RESULT 1
 US-10-057-408-36
 : Sequence 36, Application US/10057408
 : Publication No. US20030082561A1
 : GENERAL INFORMATION:
 : APPLICANT: Sera, Takashi
 : TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
 : FILE REFERENCE: 109845.135
 : CURRENT APPLICATION NUMBER: US/10/057,408
 : PRIOR FILING DATE: 2002-01-23
 : PRIOR APPLICATION NUMBER: US 60/220,060
 : NUMBER OF SEQ ID NOS: 69
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 36
 : LENGTH: 60
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Partial zinc finger domain oligomer
 : NAME/KEY: misc-feature
 : LOCATION: (45)..(56)
 : OTHER INFORMATION: Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or
 : US-10-057-408-36

Query Match 1.0%; Score 27; DB 9; Length 60;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1593 GGGGAGAACCATTTGATGTAGCGAGTGTGGCGAGGCTTTACCCGGAATCAACCTG 1652
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Db 1 GGGGAGAACCCCTTAATGTCGCGAATGTGTAAAGTTTACGNNNAGCNNNNNTTG 60

RESULT 2
US-10-057-408-49

; Sequence 49, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135

; CURRENT APPLICATION NUMBER: US/10/057,408

; PRIOR FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 49

; LENGTH: 56

; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Partial zinc finger domain oligomer

US-10-057-408-49

Query Match 1.0%; Score 26.6; DB 9; Length 56;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 921 GGGGAGACCTTACATGTACAGTGTGGGAGAGACACCTTTGCGCAGTA 969
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RESULT 3
US-10-057-408-45

; Sequence 45, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135

; CURRENT APPLICATION NUMBER: US/10/057,408

; PRIOR FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 45

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Partial zinc finger domain oligomer

US-10-057-408-45

Query Match 0.9%; Score 25.8; DB 9; Length 60;
Best Local Similarity 73.3%; Pred. No. 3.3e+02;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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RESULT 4
US-10-057-408-40

; Sequence 40, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135

; CURRENT APPLICATION NUMBER: US/10/057,408

; PRIOR FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 40

; LENGTH: 56

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Partial zinc finger domain oligomer

; NAME/KEY: misc.feature

; LOCATION: (48)..(58)

; OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or

US-10-057-408-40

Query Match 0.9%; Score 25.6; DB 9; Length 56;
Best Local Similarity 72.1%; Pred. No. 3.7e+02;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1179 AAGCCTTATGTGTCAGAGAAATGTGGCAGAGCTTTAGCCCTGA 1221
|||||
Db 7 AAGCCTTACAGTGTGCGCGAAGACCTTTAGTNNNA 49

RESULT 5
US-09-898-556A-6

; Sequence 6, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:

; APPLICANT: Susan M. Brenner

; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION

; FILE REFERENCE: RTS-0248

; CURRENT APPLICATION NUMBER: US/09/898,556A

; NUMBER OF SEQ ID NOS: 89

; SEQ ID NO 6

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: PCR Probe

US-09-898-556A-6

Query Match 0.9%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2309 CTGCCCTTCCTCAGCTGTGATGCTG 2333
|||||
Db 1 CTGCCCTTCCTCAGCTGTGATGCTG 25

RESULT 6
US-10-057-408-50/C

; Sequence 50, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135

; CURRENT APPLICATION NUMBER: US/10/057,408

; PRIOR FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 40

; LENGTH: 56

; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Partial zinc finger domain oligomer

US-10-057-408-50/C

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; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-10-057-408-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 9; Length 55;
Pred. No. 7.9e+02;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1211 CTTTACCTGAGTCAACCTCTTACCCACGAGGCGGCACCTGGGAGAG 1265
DB 55 CTTTACTGCTAGTATGATGCTTACCAACCCACGACGACGCGGGAGAG 1

RESULT 7
US-09-775-049-14/c
; Sequence 14, Application US/09775049
; Publication No. US20030036641A1
; GENERAL INFORMATION:
; APPLICANT: Padgett, Hal S.
; APPLICANT: Fitzmaurice, Wayne P.
; APPLICANT: Lindbo, John A.
; TITLE OF INVENTION: Methods For Homology-Driven Reassembly
; FILE REFERENCE: P-Lg 4412
; CURRENT APPLICATION NUMBER: US/09/775,049
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-775-049-14

Query Match
Best Local Similarity 0.9%; Score 24; DB 9; Length 58;
Pred. No. 1.3e+03;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 2219 ATTCTGTGTGATTATGATGAGACTGTACTGTAGATTTGATCT 2266
DB 55 ATCTGTGAGTAACATATGCTTAATAATATGTACTGATGGACATTTATCT 8

RESULT 8
US-10-057-408-41/c
; Sequence 41, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/10/057,408
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
NAME/KEY: misc.feature
LOCATION: (28)..(48)
```

```

; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" -
; OTHER INFORMATION: 9, a, t, or c
US-10-057-408-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 9; Length 55;
Pred. No. 1.5e+03;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1547 CTTTACCTGAGTCAACCTTTTACCAACACGAGGTACACGCGGGAGAG 1601
DB 55 CTTTACTNNNAGTNNNNNNNTTACANNNCACGACGACGCGGGAGAG 1

RESULT 9
US-09-906-393A-34
; Sequence 34, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-906-393A-34

Query Match
Best Local Similarity 0.8%; Score 23; DB 9; Length 60;
Pred. No. 2.9e+03;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 89 TCAGATCCGCGCGCTGCACCCGCTTCATCTGCTCTGAGACTT 135
DB 6 TCTGATCCGAGGTGATGATGCTTACACACGCTTCGAGCTT 52

RESULT 10
US-10-055-713-24
; Sequence 24, Application US/10055713
; Publication No. US20030044957A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: Li, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; FILE REFERENCE: 8325-0026 / 526-US1
; CURRENT APPLICATION NUMBER: US/10/055,713
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide PB2
US-10-055-713-24

Query Match
Best Local Similarity 0.8%; Score 22.4; DB 9; Length 54;
Pred. No. 4.2e+03;
```


NUMBER OF SEQ ID NOS: 89
SEQ ID NO 4
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-898-556a-4

Query Match 0.8%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2276 TGAAGAGAATTGCTGCTCA 2296
DB 1 TGAAGAGAATTGCTGCTCA 21

RESULT 16
US-09-801-274-1402
Sequence 1402, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1402
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-1402

Query Match 0.8%; Score 21; DB 10; Length 31;
Best Local Similarity 77.4%; Pred. No. 8.6e+03;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1358 TTGCAGGAGTGTGAGCAAGCCTTAGCCAG 1388
DB 1 TTGCAGGAGTGTGAGCAAGCCTTAGCCAG 31

RESULT 17
US-10-057-408-56/c
Sequence 56, Application US/10057408
Publication No. US20030082561A1
GENERAL INFORMATION:
APPLICANT: Seta, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845.135
CURRENT APPLICATION NUMBER: US/10/057,408
CURRENT FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.0
SEQ ID NO 56
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-10-057-408-56

Query Match 0.8%; Score 21; DB 9; Length 45;
Best Local Similarity 82.8%; Pred. No. 1.1e+04;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1239 CACCAAGAGCGGCACACTGGGAGAGGCC 1267
DB 45 CACCAAGAGCGGCACACTGGGAGAGGCC 17

RESULT 18
US-10-066-960-236
Sequence 236, Application US/10066960
Publication No. US20030049644A1
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/066,960
FILING DATE: 04-Feb-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,793
FILING DATE: 1999-DEC-03
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-F uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 236:
US-10-066-960-236

Query Match 0.8%; Score 21; DB 9; Length 59;
Best Local Similarity 62.2%; Pred. No. 1.3e+04;
Matches 28; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 140 CTCTCCAGAGAGACACACAGAGAGCAAGAAATGCTACAG 184

[illegible]

```

1 Publication No. US20030049644A1
2
3 GENERAL INFORMATION:
4 APPLICANT: PARMA, et al.
5
6 TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
7
8 TO LECTINS
9
10 NUMBER OF SEQUENCES: 390
11
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Swanson & Bratschun, L.L.C.
14 STREET: 8400 E. Prentice Avenue, Suite 200
15 CITY: Englewood
16 STATE: Colorado
17 COUNTRY: USA
18 ZIP: 80111
19
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
22 COMPUTER: IBM pc compatible
23 OPERATING SYSTEM: MS-DOS
24 SOFTWARE: Wordperfect 6.0
25
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/10/066,960
28 FILING DATE: 04-Feb-2002
29 CLASSIFICATION: <Unknown>
30
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 08/952,793
33 FILING DATE: 1999-DEC-03
34
35 APPLICATION NUMBER: PCT/US96/09455
36 FILING DATE: 05-JUNE-1995
37
38 APPLICATION NUMBER: 08/479,724
39 FILING DATE: 07-JUNE-1995
40
41 APPLICATION NUMBER: 08/472,256
42 FILING DATE: 07-JUNE-1995
43
44 APPLICATION NUMBER: 08/472,255
45 FILING DATE: 07-JUNE-1995
46
47 APPLICATION NUMBER: 08/477,829
48 FILING DATE: 07-JUNE-1995
49
50 ATTORNEY/AGENT INFORMATION:
51 NAME: Barry J. Swanson
52
53 REGISTRATION NUMBER: 33,215
54 REFERENCE/DOCKET NUMBER: NEX40C/PCT
55
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: (303) 793-3333
58 TELEFAX: (303) 793-3433
59
60 INFORMATION FOR SEQ. ID NO: 244:
61
62 SEQUENCE CHARACTERISTICS:
63 LENGTH: 52 base pairs
64 TYPE: nucleic acid
65 STRANDEDNESS: single
66 TOPOLOGY: linear
67
68 MOLECULE TYPE: RNA
69
70 FEATURE:
71
72 OTHER INFORMATION: All C's are 2'-F cytosine
73
74 FEATURE:
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76 OTHER INFORMATION: All U's are 2'-F uracil
77
78 SEQUENCE DESCRIPTION: SEQ ID NO: 244:
79
80 US-10-066-960-244
81
82 Query Match 0.7%; Score 20.6; DB 9; Length 52;
83 Best Local Similarity 65.7%; Pred.No.1.7e+04;
84 Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
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us-09-898-556a-3.szm60.rnpb

```

NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,928
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,793
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEK40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-F uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 244:
US-09-849-928-244

Query Match          0.7%: Score 20.6; DB 9; Length 52;
Best Local Similarity 65.7%; Pred. No. 1.7e+04;
Matches      23: Conservative   3; Mismatches    9; Indels    0; Gaps    0;

OY       580 CAGAGAATCAGAAACAACAGCAGGATCCATCTGC 614
Db        4 CAAGCGGUCAGAAACAUAAGCUGCAUACUACC GC 38

RESULT 22
US-09-950-442-40/C
Sequence 40, Application US/09950442
Publication No. US20030027127A1
GENERAL INFORMATION:
APPLICANT: Farr, Spencer B.
TITLE OF INVENTION: Todd, Marique D
METHODS AND DIAGNOSTIC KITS FOR DETERMINING TOXICITY
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr. C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York

```

```

Query Match      0.7%: Score 20.2; DB 9; Length 50;
Best Local Similarity 68.3%; Pred. No. 2.2e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0

QY      2212 TGGAGACATTCTGTGTGATTATCATGACACTGACTAGCG 2252
      || ||||| ||| |||| | | | |||| || ||||
Db      48 TCCAGACATCTACTAGTGTGCACCGCTTGACAGACAGTGGACTGG 8

US-09-898-556A-12/c
; Sequence 12, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-12

Query Match      0.7%: Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 GCTTCCTCTTAAAGTCTTT 52
      ||||| ||||| ||||| |||||
Db      20 GCTTCCTCTTAAAGTCTTT 1

RESULT 24
US-09-898-556A-13/c
Sequence 13, Application US/09898556A

```



```
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-18

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 397 AGGAGAGAAATGTCCTGCTG 416
Db 20 AGGAGAGAAATGTCCTGCTG 1

RESULT 30
US-09-898-556A-19/c
; Sequence 19, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-19

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 411 CCACCTGACCTCTGTCCAGA 430
Db 20 CCACCTGACCTCTGTCCAGA 1

RESULT 31
US-09-898-556A-20/c
; Sequence 20, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-20
```

```
Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 439 CAGAAATTCAGTACTGATCC 458
Db 20 CAGAAATTCAGTACTGATCC 1

RESULT 32
US-09-898-556A-21/c
; Sequence 21, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-21

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 470 GATTTCTCCAGCTCAGCAAG 489
Db 20 GATTTCTCCAGCTCAGCAAG 1

RESULT 33
US-09-898-556A-22/c
; Sequence 22, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-22

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 TCAGCAGACTCTCAGCCAC 501
Db 20 TCAGCAGACTCTCAGCCAC 1

RESULT 34
US-09-898-556A-23/c
; Sequence 23, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
US-09-898-556A-23
```

```
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 23
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-23
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 491 TCTCAGCCACATGTGTGCG 510
DB 20 TCTCAGCCACATGTGTGCG 1
```

```
RESULT 35
US-09-898-556A-24/C
Sequence 24, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 24
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-24
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 506 GTGGCTGAGTCATCTCTCTC 525
DB 20 GTGGCTGAGTCATCTCTCTC 1
```

```
RESULT 36
US-09-898-556A-25/C
Sequence 25, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 25
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-25
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 535 CAACTTATGGCGAGGAAT 554
DB 20 CAACTTATGGCGAGGAAT 1
```

```
RESULT 37
US-09-898-556A-26/C
Sequence 26, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 26
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-26
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 594 CAACAGCAGATCCATCTCTG 613
DB 20 CAACAGCAGATCCATCTCTG 1
```

```
RESULT 38
US-09-898-556A-27/C
Sequence 27, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 27
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-27
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 618 AGTGGCAAGCAGATGAT 637
DB 20 AGTGGCAAGCAGATGAT 1
```

```
RESULT 39
US-09-898-556A-28/C
Sequence 28, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
```

```

; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-28

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 GGGAGAGACTCCAGACTCC 663
Db 20 GGGAGAGACTCCAGACTCC 1

RESULT 40
US-09-898-556A-29/c
; Sequence 29, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-29

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 TCCAGACTCCTGTTGGAG 673
Db 20 TCCAGACTCCTGTTGGAG 1

RESULT 41
US-09-898-556A-30/c
; Sequence 30, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-30

Query Match
0.7%; Score 20; DB 9; Length 20;
Score 20; DB 9; Length 20;
```

```

Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 CAAAATGGCAGCTTCAAGG 699
Db 20 CAAAATGGCAGCTTCAAGG 1

RESULT 42
US-09-898-556A-31/c
; Sequence 31, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-31

Query Match
0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 ATGCACCTTCAAGCAGCTT 704
Db 20 ATGCACCTTCAAGCAGCTT 1

RESULT 43
US-09-898-556A-32/c
; Sequence 32, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-32

Query Match
0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 720 GAACAACAGCCAGCAGTC 739
Db 20 GAACAACAGCCAGCAGTC 1

RESULT 44
US-09-898-556A-33/c
; Sequence 33, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
```



```
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-33

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GCACAGTCCAGGAAGACAA 751
Db 20 GCACAGTCCAGGAAGACAA 1

RESULT 45
US-09-898-556A-34/c
; Sequence 34, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-34

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 ACACAGTGTGATATAGG 770
Db 20 ACACAGTGTGATATAGG 1

RESULT 46
US-09-898-556A-35/c
; Sequence 35, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-35

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 760 TGGATATAGGTCACGCCCT 779
Db 20 TGGATATAGGTCACGCCCT 1

RESULT 47
US-09-898-556A-36/c
; Sequence 36, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-36

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 GGCAGATCTAGAGAAACAG 807
Db 20 GGCAGATCTAGAGAAACAG 1

RESULT 48
US-09-898-556A-37/c
; Sequence 37, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-37

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 TGGCCAGCCTTATCAAG 885
Db 20 TGGCCAGCCTTATCAAG 1

RESULT 49
US-09-898-556A-38/c
; Sequence 38, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
```

FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO: 38
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-38

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 878 TATCAAGAGTCAACCTCC 897
DB 20 TATCAAGAGTCAACCTCC 1

RESULT 50
US-09-898-556A-39/c
Sequence 39, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO: 39
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-39

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 907 AGAAGACACAACCTGGGAG 926
DB 20 AGAAGACACAACCTGGGAG 1

Search completed: June 4, 2003, 12:47:08
Job time : 411 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 07:24:51 ; Search time 132 seconds
(without alignments)
6440.212 Million cell updates/sec

Title: US-09-898-556A-3
Perfect score: 2772
Sequence: 1 caggcgcttaagctggtg.....ttctaccatctcaccct 2772

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 635134

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents -NA:*

- 1: /cgn2-6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2-6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2-6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2-6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2-6/ptodata/1/ina/PTUS.COMB.seq:*
- 6: /cgn2-6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21.6	0.8	41	1	US-08-294-424-6
C 2	21	0.8	50	3	US-08-388-029A-30
C 3	21	0.8	52	4	US-08-906-156A-72
C 4	21	0.8	59	4	US-08-952-793-236
C 5	21	0.8	59	5	PCT-US96-09455A-236
C 6	20.8	0.8	48	2	US-08-369-829A-7
C 7	20.8	0.8	48	2	US-08-586-676E-11
C 8	20.6	0.7	47	4	US-09-641-638-1290
C 9	20.6	0.7	52	4	US-08-952-793-244
C 10	20.6	0.7	52	5	PCT-US96-09455A-244
C 11	20.2	0.7	50	1	US-08-374-641-40
C 12	20.2	0.7	52	2	US-08-553-619B-13
C 13	20.2	0.7	53	1	US-08-242-035A-2
C 14	20.2	0.7	60	1	US-08-477-270-21
C 15	20	0.7	48	1	US-08-758-626-23
C 16	20	0.7	48	5	PCT-US94-07684-23
C 17	20	0.7	55	1	US-08-173-968-7
C 18	20	0.7	55	3	US-07-801-814D-7
C 19	19.8	0.7	47	3	US-08-726-807B-21
C 20	19.8	0.7	47	3	US-09-258-367-21
C 21	19.8	0.7	47	4	US-09-546-550-21
C 22	19.8	0.7	47	4	US-09-431-414-21
C 23	19.8	0.7	47	4	US-09-225-670-21
C 24	19.8	0.7	47	4	US-09-431-348C-21
C 25	19.8	0.7	57	3	US-08-863-813A-47
C 26	19.8	0.7	59	4	US-09-037-990B-60
C 27	19.6	0.7	56	1	US-08-461-184-9

C 28	19.6	0.7	56	1	US-08-463-675-9	Sequence 9, Appli
C 29	19.6	0.7	56	1	US-08-464-589-9	Sequence 9, Appli
C 30	19.6	0.7	60	4	US-08-406-030A-8	Sequence 8, Appli
C 31	19.6	0.7	60	4	US-08-406-030A-9	Sequence 9, Appli
C 32	19.4	0.7	33	4	US-08-169-715-14	Sequence 14, Appli
C 33	19.4	0.7	43	2	US-08-417-210A-99	Sequence 99, Appli
C 34	19.4	0.7	47	4	US-09-641-638-760	Sequence 760, App
C 35	19.4	0.7	56	2	US-08-417-210A-106	Sequence 106, App
C 36	19.2	0.7	41	3	US-08-973-965-1	Sequence 1, Appli
C 37	19.2	0.7	44	3	US-08-444-818-229	Sequence 229, App
C 38	19.2	0.7	45	1	US-08-171-389-100	Sequence 100, App
C 39	19.2	0.7	45	1	US-08-123-936-100	Sequence 100, App
C 40	19.2	0.7	45	2	US-08-475-228A-100	Sequence 100, App
C 41	19.2	0.7	45	3	US-08-482-060A-100	Sequence 100, App
C 42	19.2	0.7	45	4	US-09-354-947-100	Sequence 100, App
C 43	19.2	0.7	45	5	PCT-US93-12388-100	Sequence 100, App
C 44	19.2	0.7	48	2	US-08-859-649-10	Sequence 10, Appli
C 45	19.2	0.7	48	4	US-08-207-861-10	Sequence 10, Appli
C 46	19.2	0.7	58	2	US-08-431-527A-6	Sequence 6, Appli
C 47	19.2	0.7	59	4	US-08-485-355B-53	Sequence 53, Appli
C 48	19.2	0.7	38	1	US-08-373-124A-185	Sequence 185, App
C 49	19	0.7	38	1	US-08-435-628-185	Sequence 185, App
C 50	19	0.7	46	4	US-09-609-816-13	Sequence 13, App
C 51	19	0.7	57	4	US-08-869-380-6	Sequence 6, Appli
C 52	19	0.7	57	5	PCT-US95-13552-17	Sequence 17, Appli
C 53	18.8	0.7	40	4	US-09-359-304B-34	Sequence 34, Appli
C 54	18.8	0.7	43	1	US-08-253-877C-34	Sequence 34, Appli
C 55	18.8	0.7	43	1	US-08-253-877C-35	Sequence 35, Appli
C 56	18.8	0.7	43	2	US-08-452-164A-34	Sequence 34, Appli
C 57	18.8	0.7	43	2	US-08-452-164A-35	Sequence 35, Appli
C 58	18.8	0.7	49	1	US-08-105-463-378	Sequence 378, App
C 59	18.8	0.7	49	1	US-08-709-209-378	Sequence 378, App
C 60	18.8	0.7	49	1	US-08-458-101-378	Sequence 378, App
C 61	18.8	0.7	49	2	US-08-619-362A-6	Sequence 6, Appli
C 62	18.8	0.7	54	1	US-08-227-688-3	Sequence 3, Appli
C 63	18.8	0.7	54	4	US-09-368-169-3	Sequence 3, Appli
C 64	18.8	0.7	54	4	US-09-424-620B-14	Sequence 14, Appli
C 65	18.8	0.7	60	6	5194596-31	Patent No. 5194596
C 66	18.6	0.7	60	6	5219739-36	Patent No. 5219739
C 67	18.6	0.7	25	4	US-09-150-766-6	Sequence 6, Appli
C 68	18.6	0.7	36	1	US-08-311-488C-288	Sequence 288, App
C 69	18.6	0.7	38	4	US-09-084-120-15	Sequence 15, Appli
C 70	18.6	0.7	42	2	US-08-627-151A-17	Sequence 17, Appli
C 71	18.6	0.7	47	4	US-08-569-147-17	Sequence 17, Appli
C 72	18.6	0.7	48	1	US-08-017-570-16	Sequence 16, Appli
C 73	18.6	0.7	48	1	US-08-471-426-16	Sequence 16, Appli
C 74	18.6	0.7	48	5	PCT-US94-01709-16	Sequence 16, Appli
C 75	18.6	0.7	57	2	US-08-149-097D-25	Sequence 25, Appli
C 76	18.4	0.7	31	4	US-09-248-588-18	Sequence 18, Appli
C 77	18.4	0.7	42	1	US-08-375-116A-39	Sequence 39, Appli
C 78	18.4	0.7	42	4	US-09-250-580-4	Sequence 4, Appli
C 79	18.4	0.7	45	4	US-09-291-902-3	Sequence 3, Appli
C 80	18.4	0.7	49	1	US-08-222-177A-361	Sequence 361, App
C 81	18.4	0.7	50	1	US-08-486-137-4	Sequence 4, Appli
C 82	18.4	0.7	50	1	US-08-485-180-4	Sequence 4, Appli
C 83	18.4	0.7	50	1	US-08-419-765-4	Sequence 4, Appli
C 84	18.4	0.7	51	2	US-08-704-682-8	Sequence 2, Appli
C 85	18.4	0.7	53	5	PCT-US92-09955-15	Sequence 15, Appli
C 86	18.4	0.7	54	2	US-08-448-418-70	Sequence 70, Appli
C 87	18.4	0.7	54	2	US-08-448-418-71	Sequence 71, Appli
C 88	18.2	0.7	34	2	US-08-765-782A-30	Sequence 30, Appli
C 89	18.2	0.7	34	3	US-08-921-100-30	Sequence 30, Appli
C 90	18.2	0.7	34	3	US-08-880-144-30	Sequence 30, Appli
C 91	18.2	0.7	34	3	US-08-902-201-30	Sequence 30, Appli
C 92	18.2	0.7	34	4	US-09-416-357-30	Sequence 30, Appli
C 93	18.2	0.7	42	2	US-08-658-665-135	Sequence 135, App
C 94	18.2	0.7	42	4	US-08-796-611-111	Sequence 111, App
C 95	18.2	0.7	42	4	US-09-085-273-135	Sequence 135, App
C 96	18.2	0.7	43	4	US-09-489-979-2	Sequence 2, Appli
C 97	18.2	0.7	47	4	US-08-976-183A-11	Sequence 11, Appli
C 98	18.2	0.7	48	4	US-08-952-793-194	Sequence 194, App
C 99	18.2	0.7	48	4	US-09-302-620B-68	Sequence 68, Appli
C 100	18.2	0.7	48	4	US-09-569-572C-24	Sequence 24, Appli

101	18.2	0.7	48	5	PCT-US96-09455A-194	Sequence 194, App	c 174	17.8	0.6	38	1	US-08-435-628-189	Sequence 189, App
102	18.2	0.7	50	1	US-08-207-901-41	Sequence 41, Appl	175	17.8	0.6	38	4	US-09-262-773-118	Sequence 118, App
103	18.2	0.7	50	4	US-09-315-886C-13	Sequence 13, Appl	176	17.8	0.6	43	1	US-08-560-313A-8	Sequence 8, Appl
c 104	18.2	0.7	51	4	US-09-330-245A-4	Sequence 4, Appl	177	17.8	0.6	43	1	US-08-611-155B-12	Sequence 12, Appl
105	18.2	0.7	59	2	US-08-308-887A-5	Sequence 5, Appl	177	17.8	0.6	43	1	US-08-916-120A-14	Sequence 14, Appl
106	18.2	0.7	59	3	US-08-881-094-5	Sequence 5, Appl	179	17.8	0.6	43	2	US-08-358-627E-2	Sequence 2, Appl
107	18.2	0.7	60	3	US-08-545-860D-74	Sequence 74, Appl	179	17.8	0.6	45	4	US-09-315-793-4	Sequence 4, Appl
108	18.2	0.7	60	3	US-08-658-136-26	Sequence 26, Appl	180	17.8	0.6	45	4	US-09-027-998A-5	Sequence 5, Appl
c 109	18.2	0.7	60	4	US-09-275-850-277	Sequence 277, App	181	17.8	0.6	45	4	US-09-020-846-58	Sequence 58, Appl
c 110	18.2	0.7	60	4	US-08-290-736C-29	Sequence 29, Appl	182	17.8	0.6	45	4	US-08-465-712C-2	Sequence 2, Appl
c 111	18.2	0.7	60	5	PCT-US94-04496-74	Sequence 74, Appl	183	17.8	0.6	45	4	US-09-552-733-2	Sequence 2, Appl
c 112	18.2	0.6	35	1	US-07-832-905B-24	Sequence 24, Appl	184	17.8	0.6	45	4	US-08-296-880-6	Sequence 6, Appl
c 113	18.2	0.6	35	2	US-08-700-757-24	Sequence 24, Appl	185	17.8	0.6	47	1	US-08-447-174A-6	Sequence 6, Appl
c 114	18.2	0.6	36	1	US-08-170-588-1	Sequence 1, Appl	186	17.8	0.6	47	1	US-08-434-743-1	Sequence 1, Appl
c 115	18.2	0.6	36	2	US-08-482-182-1	Sequence 1, Appl	c 187	17.8	0.6	47	1	US-08-685-793-1	Sequence 1, Appl
c 116	18.2	0.6	36	2	US-08-482-182-19	Sequence 19, Appl	c 188	17.8	0.6	47	1	US-08-685-793-8	Sequence 8, Appl
c 117	18.2	0.6	36	2	US-08-482-182-25	Sequence 25, Appl	c 189	17.8	0.6	47	1	US-08-685-793-8	Sequence 8, Appl
c 118	18.2	0.6	37	1	US-07-744-283C-43	Sequence 43, Appl	c 190	17.8	0.6	47	2	US-08-800-641-6	Sequence 6, Appl
c 119	18.2	0.6	37	5	PCT-US92-06821A-86	Sequence 86, Appl	c 191	17.8	0.6	47	3	US-08-821-524-3	Sequence 3, Appl
c 120	18.2	0.6	43	1	US-08-041-538-11	Sequence 11, Appl	c 192	17.8	0.6	47	4	US-09-613-263-3	Sequence 3, Appl
c 121	18.2	0.6	43	1	US-08-463-642-11	Sequence 11, Appl	c 193	17.8	0.6	49	4	US-09-641-638-671	Sequence 671, App
c 122	18.2	0.6	43	1	US-08-455-602-11	Sequence 11, Appl	c 194	17.8	0.6	49	4	US-09-358-972-117	Sequence 117, App
c 123	18.2	0.6	43	5	US-08-465-157-11	Sequence 11, Appl	c 195	17.8	0.6	49	4	US-09-358-972-118	Sequence 118, App
c 124	18.2	0.6	43	5	PCT-US91-05177-9	Sequence 9, Appl	c 196	17.8	0.6	49	4	US-09-383-316-16	Sequence 16, App
c 125	18.2	0.6	43	5	PCT-US91-09422-11	Sequence 11, Appl	c 197	17.8	0.6	49	4	US-09-383-316-17	Sequence 17, App
c 126	18.2	0.6	45	1	US-08-171-389-296	Sequence 296, App	c 198	17.8	0.6	49	4	US-09-609-816-14	Sequence 14, Appl
c 127	18.2	0.6	45	1	US-08-233-009-43	Sequence 43, Appl	c 199	17.8	0.6	50	2	US-08-867-579-1	Sequence 1, Appl
c 128	18.2	0.6	45	1	US-08-123-936-296	Sequence 296, App	c 200	17.8	0.6	51	4	US-09-460-303-4	Sequence 4, Appl
c 129	18.2	0.6	45	2	US-08-475-228A-296	Sequence 296, App	c 201	17.8	0.6	52	4	US-09-506-729-11	Sequence 11, Appl
c 130	18.2	0.6	45	3	US-08-482-080A-296	Sequence 296, App	c 202	17.8	0.6	53	4	US-09-275-850-267	Sequence 267, App
c 131	18.2	0.6	45	4	US-09-354-947-296	Sequence 296, App	c 203	17.8	0.6	53	4	US-09-275-850-269	Sequence 269, App
c 132	18.2	0.6	45	5	PCT-US93-12388-296	Sequence 296, App	c 204	17.8	0.6	53	4	US-09-813-781-89	Sequence 89, Appl
c 133	18.2	0.6	46	4	US-09-380-190A-63	Sequence 63, Appl	c 205	17.8	0.6	53	4	US-09-813-781-94	Sequence 94, Appl
c 134	18.2	0.6	47	4	US-09-641-638-769	Sequence 769, App	c 206	17.8	0.6	54	1	US-08-081-539-57	Sequence 57, Appl
c 135	18.2	0.6	47	4	US-09-641-638-1113	Sequence 1113, App	c 207	17.8	0.6	54	1	US-08-466-647-57	Sequence 57, Appl
c 136	18.2	0.6	48	2	US-08-477-553A-13	Sequence 13, Appl	c 208	17.8	0.6	54	1	US-08-279-058B-12	Sequence 12, Appl
c 137	18.2	0.6	49	1	US-08-483-883-72	Sequence 72, Appl	c 209	17.8	0.6	54	1	US-08-273-534-13	Sequence 13, Appl
c 138	18.2	0.6	49	1	US-08-483-883-72	Sequence 72, Appl	c 210	17.8	0.6	54	1	US-08-311-486C-14	Sequence 14, Appl
c 139	18.2	0.6	49	2	US-08-484-993B-57	Sequence 57, Appl	c 211	17.8	0.6	54	2	US-08-773-297-24	Sequence 24, Appl
c 140	18.2	0.6	49	2	US-08-487-113D-72	Sequence 72, Appl	c 212	17.8	0.6	54	3	US-09-098-293-24	Sequence 24, Appl
c 141	18.2	0.6	49	2	US-08-473-503-72	Sequence 72, Appl	c 213	17.8	0.6	54	3	US-09-094-919-13	Sequence 13, Appl
c 142	18.2	0.6	49	2	US-08-483-932-72	Sequence 72, Appl	c 214	17.8	0.6	54	4	US-09-506-729-17	Sequence 17, App
c 143	18.2	0.6	49	2	US-08-484-156B-57	Sequence 57, Appl	c 215	17.8	0.6	54	4	US-08-828-323-12	Sequence 12, Appl
c 144	18.2	0.6	49	2	US-08-484-556A-57	Sequence 57, Appl	c 216	17.8	0.6	54	4	US-09-438-954-29	Sequence 29, Appl
c 145	18.2	0.6	49	2	US-08-480-150A-57	Sequence 57, Appl	c 217	17.8	0.6	57	1	US-08-530-492-107	Sequence 107, App
c 146	18.2	0.6	49	2	US-08-720-420A-72	Sequence 72, Appl	c 218	17.8	0.6	57	4	US-08-906-517-107	Sequence 107, App
c 147	18.2	0.6	49	3	US-08-458-731-57	Sequence 57, Appl	c 219	17.8	0.6	58	1	US-08-076-094A-9	Sequence 9, Appl
c 148	18.2	0.6	49	3	US-08-149-223A-57	Sequence 57, Appl	c 220	17.8	0.6	58	4	US-09-439-897-42	Sequence 42, Appl
c 149	18.2	0.6	49	3	US-08-714-017-72	Sequence 72, Appl	c 221	17.8	0.6	58	5	PCT-US94-06132-9	Sequence 9, Appl
c 150	18.2	0.6	49	3	US-08-475-680-72	Sequence 72, Appl	c 222	17.8	0.6	59	2	US-08-704-473-23	Sequence 23, Appl
c 151	18.2	0.6	51	3	US-08-930-503A-14	Sequence 14, Appl	c 223	17.8	0.6	60	3	US-08-658-136-24	Sequence 24, Appl
c 152	18.2	0.6	52	2	US-08-560-098A-41	Sequence 41, Appl	c 224	17.6	0.6	27	4	US-08-584-040-278	Sequence 278, App
c 153	18.2	0.6	53	3	US-08-864-473-60	Sequence 60, Appl	c 225	17.6	0.6	28	1	US-07-786-902-3	Sequence 3, Appl
c 154	18.2	0.6	53	4	US-09-440-523-60	Sequence 60, Appl	c 226	17.6	0.6	35	1	US-08-317-432A-34	Sequence 34, Appl
c 155	18.2	0.6	54	2	US-08-588-201-11	Sequence 60, Appl	c 227	17.6	0.6	35	4	US-08-646-301A-5	Sequence 5, Appl
c 156	18.2	0.6	54	2	US-09-169-605-11	Sequence 11, Appl	c 228	17.6	0.6	35	4	US-08-481-968A-9	Sequence 9, Appl
c 157	18.2	0.6	54	3	US-08-893-327-11	Sequence 11, Appl	c 229	17.6	0.6	35	4	US-08-154-712B-9	Sequence 9, Appl
c 158	18.2	0.6	54	4	US-08-706-945D-69	Sequence 69, Appl	c 230	17.6	0.6	36	1	US-07-781-254A-27	Sequence 27, Appl
c 159	18.2	0.6	55	2	US-08-774-065-8	Sequence 8, Appl	c 231	17.6	0.6	36	1	US-08-311-760A-91	Sequence 91, Appl
c 160	18.2	0.6	55	2	US-07-609-716-72	Sequence 72, Appl	c 232	17.6	0.6	36	2	US-08-441-887A-7	Sequence 7, Appl
c 161	18.2	0.6	60	3	US-08-475-411A-72	Sequence 72, Appl	c 233	17.6	0.6	36	2	US-08-585-664B-1864	Sequence 1864, App
c 162	18.2	0.6	60	4	US-08-478-029A-72	Sequence 256, App	c 234	17.6	0.6	36	2	US-08-774-310-91	Sequence 91, App
c 163	18.2	0.6	60	4	US-09-275-850-256	Sequence 26, Appl	c 235	17.6	0.6	36	3	US-08-544-381B-113	Sequence 113, App
c 164	18.2	0.6	60	4	US-07-963-475-6	Sequence 6, Appl	c 236	17.6	0.6	36	4	US-09-038-073-1864	Sequence 1864, App
c 165	17.8	0.6	22	4	US-09-289-368-2	Sequence 2, Appl	c 237	17.6	0.6	37	4	US-07-875-790B-11	Sequence 11, Appl
c 166	17.8	0.6	30	1	US-08-186-229-47	Sequence 47, Appl	c 238	17.6	0.6	39	4	US-09-281-481A-11	Sequence 11, Appl
c 167	17.8	0.6	30	2	US-08-470-124-47	Sequence 47, Appl	c 239	17.6	0.6	41	1	US-08-294-424-20	Sequence 20, Appl
c 168	17.8	0.6	30	2	US-09-129-686-8	Sequence 8, Appl	c 240	17.6	0.6	42	4	US-09-382-616A-25	Sequence 25, Appl
c 169	17.8	0.6	32	4	US-09-566-581-8	Sequence 8, Appl	c 241	17.6	0.6	43	2	US-08-756-506-19	Sequence 19, Appl
c 170	17.8	0.6	38	1	US-08-373-124A-177	Sequence 177, App	c 242	17.6	0.6	43	4	US-08-057-430A-9	Sequence 9, Appl
c 171	17.8	0.6	38	1	US-08-373-124A-189	Sequence 189, App	c 243	17.6	0.6	45	1	US-08-171-389-185	Sequence 185, App
c 172	17.8	0.6	38	1	US-08-435-628-177	Sequence 177, App	c 244	17.6	0.6	45	1	US-08-123-936-185	Sequence 185, App
c 173	17.8	0.6	38	1	US-08-435-628-177	Sequence 177, App	c 245	17.6	0.6	45	1	US-08-253-877C-37	Sequence 37, App
							c 246	17.6	0.6	45	1		

247	17.6	0.6	45	2	US-08-475-228A-185	Sequence 185, App	C 320	17.4	0.6	47	3	US-08-482-080A-4	Sequence 4, Appl
248	17.6	0.6	45	2	US-08-452-164A-37	Sequence 37, Appl	C 321	17.4	0.6	47	4	US-09-349-644-8	Sequence 8, Appl
249	17.6	0.6	45	3	US-08-482-080A-185	Sequence 185, App	C 322	17.4	0.6	47	4	US-09-354-947-4	Sequence 4, Appl
250	17.6	0.6	45	3	US-08-864-473-70	Sequence 70, Appl	C 323	17.4	0.6	47	4	US-09-641-638-820	Sequence 820, Appl
251	17.6	0.6	45	4	US-09-440-523-70	Sequence 23, Appl	C 324	17.4	0.6	47	4	US-09-641-638-1264	Sequence 1264, Ap
C 252	17.6	0.6	45	4	US-09-069-821-23	Sequence 23, Appl	C 325	17.4	0.6	49	5	PCT-US93-12388-4	Sequence 4, Appl
253	17.6	0.6	45	4	US-09-354-947-185	Sequence 185, App	C 326	17.4	0.6	49	5	US-08-706-135-5	Sequence 5, Appl
254	17.6	0.6	45	5	PCT-US93-12388-185	Sequence 185, App	C 327	17.4	0.6	49	5	PCT-US95-16904-5	Sequence 5, Appl
C 255	17.6	0.6	46	5	PCT-US95-11684-24	Sequence 24, Appl	C 328	17.4	0.6	52	1	US-08-301-872A-11	Sequence 11, Appl
256	17.6	0.6	47	1	US-08-222-177A-458	Sequence 458, App	C 329	17.4	0.6	52	1	US-08-301-872A-11	Sequence 11, Appl
257	17.6	0.6	47	1	US-09-641-638-1167	Sequence 1167, Ap	C 330	17.4	0.6	52	2	US-08-443-372A-11	Sequence 11, Appl
C 258	17.6	0.6	49	2	US-08-756-506-18	Sequence 18, Appl	C 331	17.4	0.6	52	2	US-08-443-372A-11	Sequence 11, Appl
C 259	17.6	0.6	49	4	US-08-849-567A-69	Sequence 69, Appl	C 332	17.4	0.6	52	2	US-08-443-372A-12	Sequence 12, Appl
C 260	17.6	0.6	49	4	US-09-206-942-95	Sequence 95, Appl	C 333	17.4	0.6	53	1	US-08-770-233A-65	Sequence 65, Appl
C 261	17.6	0.6	50	1	US-08-207-901-78	Sequence 78, Appl	C 334	17.4	0.6	53	1	US-08-429-181-12	Sequence 12, Appl
C 262	17.6	0.6	50	2	US-08-860-174A-22	Sequence 22, Appl	C 335	17.4	0.6	53	1	US-08-164-388-12	Sequence 12, Appl
C 263	17.6	0.6	50	4	US-08-646-695-10	Sequence 10, Appl	C 336	17.4	0.6	54	2	US-08-448-418-72	Sequence 72, Appl
C 264	17.6	0.6	50	4	US-09-171-025-21	Sequence 21, Appl	C 337	17.4	0.6	57	1	US-07-911-531-12	Sequence 12, Appl
C 265	17.6	0.6	50	4	US-08-906-156A-71	Sequence 71, Appl	C 338	17.4	0.6	57	3	US-07-693-636A-12	Sequence 12, Appl
C 266	17.6	0.6	50	5	PCT-US95-13975-59	Sequence 59, Appl	C 339	17.4	0.6	57	4	US-09-159-274-1	Sequence 1, Appl
C 267	17.6	0.6	50	5	PCT-US96-06053-10	Sequence 10, Appl	C 340	17.4	0.6	57	4	US-09-461-697-147	Sequence 147, App
C 268	17.6	0.6	51	1	US-08-208-886C-52	Sequence 52, Appl	C 341	17.4	0.6	57	4	US-09-238-356-7	Sequence 7, Appl
C 269	17.6	0.6	51	1	US-08-704-744-52	Sequence 52, Appl	C 342	17.4	0.6	58	1	US-08-332-420-47	Sequence 47, Appl
C 270	17.6	0.6	51	1	US-08-469-357-52	Sequence 52, Appl	C 343	17.4	0.6	58	2	US-08-467-948A-18	Sequence 18, Appl
C 271	17.6	0.6	51	2	US-08-290-793B-52	Sequence 52, Appl	C 344	17.4	0.6	59	4	US-08-467-947A-18	Sequence 18, Appl
C 272	17.6	0.6	51	3	US-08-284-516C-26	Sequence 26, Appl	C 345	17.4	0.6	60	3	US-09-508-277C-9	Sequence 9, Appl
C 273	17.6	0.6	51	4	US-09-537-911A-26	Sequence 26, Appl	C 346	17.4	0.6	60	3	US-08-545-860D-73	Sequence 73, Appl
C 274	17.6	0.6	53	4	US-09-710-200-13	Sequence 13, Appl	C 347	17.4	0.6	60	4	US-08-643-704A-9	Sequence 9, Appl
C 275	17.6	0.6	55	4	US-09-423-439-12	Sequence 12, Appl	C 348	17.4	0.6	60	4	US-09-502-558-16	Sequence 16, Appl
C 276	17.6	0.6	55	5	PCT-US92-10024-8	Sequence 8, Appl	C 349	17.4	0.6	60	5	PCT-US94-0449-73	Sequence 73, Appl
C 277	17.6	0.6	58	2	US-08-431-527A-7	Sequence 7, Appl	C 350	17.2	0.6	25	4	US-08-943-731-509	Sequence 509, App
C 278	17.6	0.6	60	2	US-08-053-451B-121	Sequence 121, App	C 351	17.2	0.6	25	4	US-09-183-412-39	Sequence 39, Appl
C 279	17.6	0.6	60	3	US-08-911-894-64	Sequence 64, Appl	C 352	17.2	0.6	28	1	US-08-150-766-5	Sequence 5, Appl
C 280	17.6	0.6	60	3	US-08-754-681-19	Sequence 19, Appl	C 353	17.2	0.6	28	1	US-08-318-867A-19	Sequence 19, Appl
C 281	17.6	0.6	60	4	US-09-357-487B-19	Sequence 19, Appl	C 354	17.2	0.6	30	1	US-08-952-088A-5	Sequence 5, Appl
C 282	17.6	0.6	60	4	US-09-602-428-19	Sequence 19, Appl	C 355	17.2	0.6	30	1	US-08-186-223-38	Sequence 38, Appl
C 283	17.6	0.6	60	5	PCT-US96-03916-49	Sequence 49, Appl	C 356	17.2	0.6	30	2	US-08-244-466-1	Sequence 1, Appl
C 284	17.4	0.6	32	1	US-07-618-312A-6	Sequence 6, Appl	C 357	17.2	0.6	30	2	US-08-470-121-38	Sequence 38, Appl
C 285	17.4	0.6	32	1	US-08-280-228-6	Sequence 6, Appl	C 358	17.2	0.6	30	2	US-08-629-001A-116	Sequence 116, App
C 286	17.4	0.6	36	1	US-08-291-932A-516	Sequence 516, App	C 359	17.2	0.6	33	1	US-08-642-274D-195	Sequence 195, App
C 287	17.4	0.6	36	2	US-08-292-620A-1408	Sequence 1408, Ap	C 360	17.2	0.6	33	1	US-08-292-945-1	Sequence 1, Appl
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C 293	17.4	0.6	37	1	US-08-273-362-1	Sequence 1, Appl	C 366	17.2	0.6	34	4	US-08-973-131-67	Sequence 67, Appl
C 294	17.4	0.6	37	3	US-08-702-870A-17	Sequence 17, Appl	C 367	17.2	0.6	34	4	US-08-467-602-94	Sequence 94, Appl
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C 297	17.4	0.6	41	4	US-08-962-281-18	Sequence 18, Appl	C 370	17.2	0.6	36	3	US-08-685-808-12	Sequence 12, Appl
C 298	17.4	0.6	42	1	US-07-981-525-12	Sequence 12, Appl	C 371	17.2	0.6	36	4	US-08-505-860C-12	Sequence 12, Appl
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C 302	17.4	0.6	42	3	US-08-813-507-131	Sequence 131, App	C 375	17.2	0.6	38	1	US-08-435-628-187	Sequence 187, App
C 303	17.4	0.6	42	4	US-09-290-577-8	Sequence 8, Appl	C 376	17.2	0.6	38	1	US-08-435-628-187	Sequence 187, App
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C 421	17.2	0.6	50	1	US-08-171-389-558
C 422	17.2	0.6	50	1	US-08-384-708A-5
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C 433	17.2	0.6	52	4	US-09-234-874A-68
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C 436	17.2	0.6	54	4	US-08-797-812-5
C 437	17.2	0.6	55	4	US-09-357-740-18
C 438	17.2	0.6	57	4	US-08-129-722A-7
C 439	17.2	0.6	58	1	US-08-219-012-55
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C 459	17.2	0.6	36	2	US-08-585-684B-2022
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C 463	17.2	0.6	38	1	US-08-106-761-9
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Sequence 90, Appl	C 468	17	0.6	43	4	US-09-424-355-401
Sequence 113, App	C 469	17	0.6	43	4	US-08-758-417A-251
Sequence 237, App	C 470	17	0.6	44	2	US-08-331-389A-27
Sequence 237, App	C 471	17	0.6	44	2	US-08-790-963-86
Sequence 167, App	C 472	17	0.6	44	3	US-08-990-176A-2
Sequence 237, App	C 473	17	0.6	44	4	US-09-192-657A-27
Sequence 2, Appl	C 474	17	0.6	44	4	US-09-371-774-86
Sequence 237, App	C 475	17	0.6	45	1	US-08-337-268A-58
Sequence 952, App	C 476	17	0.6	45	1	US-08-484-570A-58
Sequence 965, App	C 477	17	0.6	45	2	US-08-882-756-1
Sequence 974, App	C 478	17	0.6	45	2	US-08-882-756-2
Sequence 237, App	C 479	17	0.6	45	2	US-08-882-756-5
Sequence 67, Appl	C 480	17	0.6	45	2	US-08-687-355A-12
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Sequence 67, Appl	C 482	17	0.6	45	4	US-09-301-153-2
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Sequence 67, Appl	C 484	17	0.6	45	4	US-09-218-207-259
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Sequence 67, Appl	C 486	17	0.6	46	4	US-08-977-378-19
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Sequence 34, Appl	C 489	17	0.6	47	4	US-09-641-638-1047
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Sequence 6, Appl	C 492	17	0.6	48	4	US-09-518-914-23
Sequence 5, Appl	C 493	17	0.6	48	4	US-09-002-117-18
Sequence 558, App	C 494	17	0.6	49	4	US-09-374-584-18
Sequence 558, App	C 495	17	0.6	49	4	US-09-538-709-1004
Sequence 558, App	C 496	17	0.6	49	4	US-08-974-691-14
Sequence 5, Appl	C 497	17	0.6	50	4	US-08-525-506-7
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Sequence 558, App	C 499	17	0.6	51	4	US-09-085-028-7
Sequence 337, App	C 500	17	0.6	52	3	US-08-388-022A-31

ALIGNMENTS

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RESULT 1
US-08-294-424-6/c
; Sequence 6, Application US/08294424
; Patent No. 5800984
; GENERAL INFORMATION:
; APPLICANT: Vary, Calvin
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE DETECTION BY
; TITLE OF INVENTION: TRIPLE HELIX FORMATION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,424
; FILING DATE:
; CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/000,922
; FILING DATE: 16 JAN 1993
; APPLICATION NUMBER: US/07/629,601B
; FILING DATE: 17-DEC-1990
ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066

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Sequence 4, Appl	466	17	0.6	42	3	US-08-997-758-4
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Sequence 251, App	C 469	17	0.6	43	4	US-08-758-417A-251
Sequence 27, Appl	C 470	17	0.6	44	2	US-08-331-389A-27
Sequence 86, Appl	C 471	17	0.6	44	2	US-08-790-963-86
Sequence 2, Appl	C 472	17	0.6	44	3	US-08-990-176A-2
Sequence 27, Appl	C 473	17	0.6	44	4	US-09-192-657A-27
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Sequence 58, Appl	C 475	17	0.6	45	1	US-08-337-268A-58
Sequence 1, Appl	C 476	17	0.6	45	1	US-08-484-570A-58
Sequence 2, Appl	C 477	17	0.6	45	2	US-08-882-756-1
Sequence 5, Appl	C 478	17	0.6	45	2	US-08-882-756-2
Sequence 12, Appl	C 479	17	0.6	45	2	US-08-882-756-5
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Sequence 259, App	C 482	17	0.6	45	4	US-09-301-153-2
Sequence 12, Appl	C 483	17	0.6	45	4	US-09-338-907-259
Sequence 259, App	C 484	17	0.6	45	4	US-09-218-207-259
Sequence 10, Appl	C 485	17	0.6	45	4	US-09-407-367-12
Sequence 907, App	C 486	17	0.6	46	4	US-08-977-378-19
Sequence 1080, Ap	C 487	17	0.6	47	4	US-08-976-189A-10
Sequence 23, Appl	C 488	17	0.6	47	4	US-09-641-638-907
Sequence 18, Appl	C 489	17	0.6	47	4	US-09-641-638-1047
Sequence 14, Appl	C 490	17	0.6	47	4	US-09-641-638-1080
Sequence 7, Appl	C 491	17	0.6	48	2	US-09-710-200-7
Sequence 18, Appl	C 492	17	0.6	48	4	US-09-518-914-23
Sequence 18, Appl	C 493	17	0.6	48	4	US-09-002-117-18
Sequence 1004, Ap	C 494	17	0.6	49	4	US-09-374-584-18
Sequence 7, Appl	C 495	17	0.6	49	4	US-09-538-709-1004
Sequence 31, Appl	C 496	17	0.6	49	4	US-08-974-691-14
	C 497	17	0.6	50	4	US-08-525-506-7
	C 498	17	0.6	51	2	US-08-085-028-7
	C 499	17	0.6	51	4	US-09-085-028-7
	C 500	17	0.6	52	3	US-08-388-022A-31

REFERENCE/DOCKET NUMBER: 00088-037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 41
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-424-6

Query Match 0.8%; Score 21.6; DB 1; Length 41;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 374 GCGAGGGAGAGCGCCCTGGAGAGAGAGAAAATG 409
Db 39 GCGTTGCTGATCGCCTTGAGAGAGAGAGAAAAG 4

RESULT 2
US-08-388-029A-30/C
Sequence 30, Application US/08388029A
Patent No. 6110665
GENERAL INFORMATION:
APPLICANT: FENGER, CLARA K.
APPLICANT: GRANSTROM, DAVID R.
APPLICANT: GAJADHAR, ALVIN A.
TITLE OF INVENTION: SARCOCYTIS NEURONA DIAGNOSTIC PRIMER
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: US
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388.029A
FILING DATE: 14-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PRICE, ROBERT L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 434-046
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
TELEX: AMERPAT
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-388-029A-30

Query Match 0.8%; Score 21; DB 3; Length 50;
Best Local Similarity 58.7%; Pred. No. 2.6e+03;
Matches 27; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1637 CCGGAATCAACCTGATCAGCGACAGAGACACTCAGGGAG 1682
||||| ||||||| | | | ||| || |||||

Db 50 CCGGAAGCAACCTAATNCCCNNAACNNNACAGCCAGGAG 5

RESULT 3
US-08-906-156A-72/C
Sequence 72, Application US/08906156A
Patent No. 6287854
GENERAL INFORMATION:
APPLICANT: SPURR, NIGEL K
APPLICANT: GRAY, IAN C
APPLICANT: STEWART, LORNA M
TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906.156A
FILING DATE: 05-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,655
FILING DATE: 02-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,147
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,840
FILING DATE: 23-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/96GB/02588
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1090-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: human
US-08-906-156A-72

Query Match 0.8%; Score 21; DB 4; Length 52;
Best Local Similarity 82.8%; Pred. No. 2.6e+03;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 528 CTGTTTCAAGTTTATGGGACAGGAATCC 556
Db 41 CTGCTTCAAGTCTTCTGACAGGAATCC 13
||||| ||||||| | | | |||||

RESULT 4
US-08-952-793-236
Sequence 236, Application US/08952793

Patent No. 6280932
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION/DOCKET NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-F uracil
US-08-952-793-236
Query Match 0.8%; Score 21; DB 4; Length 59;
Best Local Similarity 62.2%; Pred. No. 2.9e+03;
Matches 28; Conservative 2; Mismatches 15; Indels 0; Gaps 0;
OY 140 CTTCTCAGAGAGCACTCAGAGACCGAGAAATGGCTACAG 184
Db 1 CUCACAGAGCAAAAGUACUCACGGGACCGAGAGAUACGACACAGC 45
RESULT 5
PCT-US96-09455A-236
Sequence 236, Application PC/TUS9609455A
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
LIGANDS TO LECTINS

NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455A
FILING DATE: 05 JUNE 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION/DOCKET NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-F uracil
PCT-US96-09455A-236
Query Match 0.8%; Score 21; DB 5; Length 59;
Best Local Similarity 62.2%; Pred. No. 2.9e+03;
Matches 28; Conservative 2; Mismatches 15; Indels 0; Gaps 0;
OY 140 CTTCTCAGAGAGCACTCAGAGACCGAGAAATGGCTACAG 184
Db 1 CUCACAGAGCAAAAGUACUCACGGGACCGAGAGAUACGACACAGC 45
RESULT 6
US-08-369-829A-7
Sequence 7, Application US/08369829A
Patent No. 5861377
GENERAL INFORMATION:
APPLICANT: Hans Filtz
APPLICANT: Christian Sommerhoff
APPLICANT: Julia Helm
TITLE OF INVENTION: No. 5861377el Inhibitor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5861377artis Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey

1 RESULT 7
 2 US-08-586-676E-11
 3 Sequence 11 Application US/08586676E
 4 Patent No. 5972698
 5 GENERAL INFORMATION:
 6 APPLICANT: Fritz, Hans,
 7 APPLICANT: Sommerhoff, Christian
 8 TITLE OF INVENTION: Tryptase Inhibitor
 9 NUMBER OF SEQUENCES: 24
 10 CORRESPONDENCE ADDRESSES:
 11 ADDRESSSEE: No. 5972698artis Corporation, Patent and Trademark Department
 12 STREET: 564 Morris Avenue
 13 CITY: Summit
 14 STATE: New Jersey
 15 COUNTRY: US
 16 ZIP: 07901-1027
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: Floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC-DOS/MS-DOS
 21 SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: US/08/586,676E
 24 FILING DATE: 25-JAN-1996
 25 PRIOR APPLICATION DATA:
 26 APPLICATION NUMBER: PCT/EP94/02445
 27 FILING DATE: 25-JUL-1994
 28 PRIOR APPLICATION DATA:
 29 APPLICATION NUMBER: EP 93111930.9
 30 FILING DATE: 26-JUL-1993
 31 ATTORNEY/AGENT INFORMATION:
 32

RESULT 9
US-08-952-793-244
; Sequence 244, Application US/08952793
; Patent No. 6280832
; GENERAL INFORMATION:
; APPLICANT: PARMA, et al.

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
OTHER INFORMATION: All U's are 2'-F uracil
US-08-952-793-244
Query Match 0.7%; Score 20.6; DB 4; Length 52;
Best Local Similarity 65.7%; Pred. No. 3.6e+03;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OY 580 CAGAAGATCAGAAACACAGCAGATCCATCTGC 614
DB 4 CAAGCGGUCAGAAACAAUAGCUGAUAUACUACCCG 38
RESULT 10
PCT-US96-09455A-244
Sequence 244, Application PC/TUS9609455A
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455A
FILING DATE: 05 JUNE 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
OTHER INFORMATION: All U's are 2'-F uracil
PCT-US96-09455A-244
Query Match 0.7%; Score 20.6; DB 5; Length 52;
Best Local Similarity 65.7%; Pred. No. 3.6e+03;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OY 580 CAGAAGATCAGAAACACAGCAGATCCATCTGC 614
DB 4 CAAGCGGUCAGAAACAAUAGCUGAUAUACUACCCG 38
RESULT 11
US-08-374-641-40/C
Sequence 40, Application US/08374641
Patent No. 5811231
GENERAL INFORMATION:
APPLICANT: Fatt, Spencer B.
APPLICANT: Todd, Marque D.
TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS FOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr. c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374.641
FILING DATE: 12-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: X-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-374-641-40

Query Match 0.7%; Score 20.2; DB 1; Length 50;
Best Local Similarity 68.3%; Pred. No. 4.7e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 2212 TGAGACATCTGCTGTGATTATGATGAGACTGTACTGG 2252
DB 48 TGACAGACTAGTACTGTCACCGTTGAAGAGAGTGAGTGG 8

RESULT 12
US-08-553-619B-13
Sequence 13, Application US/08553619B
Patent No. 5919705
GENERAL INFORMATION:
APPLICANT: Dehaan, Petrus T.
TITLE OF INVENTION: Vitrus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5919705artis Crop Protection
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553.619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1082/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-1358
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
HYPOTHETICAL: NO
ORIGINAL SOURCE:

ORGANISM: oligonucleotide
US-08-553-619B-13

Query Match 0.7%; Score 20.2; DB 2; Length 52;
Best Local Similarity 63.3%; Pred. No. 4.8e+03;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 1437 TATGATGACAGACATGTGGCGCTTACTGGAATCAACCTCA 1485
DB 1 TTTCATCCAGACATGTGTGACATTTTGTATATCAACTCA 49

RESULT 13
US-08-242-035A-2
Sequence 2, Application US/08242035A
Patent No. 5545717
GENERAL INFORMATION:
APPLICANT: Weissbach, Lawrence
TITLE OF INVENTION: PLASMID AND PLASMID ANTIBODY
TITLE OF INVENTION: COMPOSITIONS AS MALIGNANT CELL MARKERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242.035A
FILING DATE: May 12, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/872.645
FILING DATE: April 21, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/116001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-242-035A-2

Query Match 0.7%; Score 20.2; DB 1; Length 53;
Best Local Similarity 68.3%; Pred. No. 4.9e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 2203 ATACCAAGTGGAGACATCTGCTGTGATTATGATGAGA 2243
DB 10 ATATCAGCTAAGACAGACAGTGTGTGATATGCTGAA 50

RESULT 14
US-08-477-270-21/C
Sequence 21, Application US/08477270
Patent No. 5629158
GENERAL INFORMATION:
APPLICANT: Uhlen, Mathias
TITLE OF INVENTION: SOLID PHASE DIAGNOSIS OF MEDICAL
TITLE OF INVENTION: CONDITIONS

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,270
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/261,010
FILING DATE:
APPLICATION NUMBER: US 07/781,157
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16787/153 DFBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
US-08-477-270-21

Query Match 0.7%; Score 20.2; DB 1; Length 60;
Best Local Similarity 63.3%; Pred. No. 5.3e+03;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 863 GTTGGCCAGCCTTATCAAGAGCTCAACCTCCTGAGCTCCAGAG 911
DB 52 GTTGAAGACACTTCTCCCGAGTCAAGTCTTGAAGCTGCAGAG 4

RESULT 15
US-08-758-626-23/c
Sequence 23, Application US/08758626
Patent No. 5736334
GENERAL INFORMATION:
APPLICANT: One Spies
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
NUMBER OF SEQUENCES: 33
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,626
FILING DATE: 27-NOV-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/422,018
FILING DATE:
APPLICATION NUMBER: 08/090,755
FILING DATE: JULY 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-758-626-23

Query Match 0.7%; Score 20; DB 1; Length 48;
Best Local Similarity 72.2%; Pred. No. 5.3e+03;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 570 AACACTATCCAGAGATCGAAGACACAGCAGGAT 605
DB 45 AAGAACCAACAGAGATGAGCATGACGACGAGAT 10

RESULT 16
PCT-US94-07684-23/c
Sequence 23, Application US/
GENERAL INFORMATION:
APPLICANT: ABBOTT LABORATORIES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
NUMBER OF SEQUENCES: 33
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,755
FILING DATE: JULY 13, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
PCT-US94-07684-23

Query Match 0.7%; Score 20; DB 5; Length 48;
Best Local Similarity 72.2%; Pred. No. 5.3e+03;

Best Local Similarity 65.9%; Pred. No. 5.8e+03;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 618 ACTGCCAAGCAGATGATTCAGAGGAGAGACTCCAGACT 661
11 11 11111 1 11111 111111111
Db 10 ACTGCCCTGCAGAGAGAGCTGAGAGATCAAGATCTCTGACT 53

RESULT 19
US-08-726-807B-21/c

; Sequence 21, Application US/08726807B
; Patent No. 6090618

; GENERAL INFORMATION:

; APPLICANT: Parmacek, Michael S.

; APPLICANT: Solway, Julian

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/726,807B

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/004,868

; FILING DATE: 05-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: McMillian, Nabeeela R.

; REGISTRATION NUMBER: P-43,363

; REFERENCE/DOCKET NUMBER: ARSB:510

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 47 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-726-807B-21

Query Match

Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 20
US-09-258-367-21/c

; Sequence 21, Application US/092586367

; Patent No. 6114311

; GENERAL INFORMATION:

; APPLICANT: PARMACEK, MICHAEL S.

; APPLICANT: SOLWAY, JULIAN

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION

; FILE REFERENCE: ARCD:310

; CURRENT APPLICATION NUMBER: US/09/258,367

; CURRENT FILING DATE: 1999-02-26

; EARLIER APPLICATION NUMBER: 08/726,807

; EARLIER FILING DATE: 1996-10-07

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 21

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; US-09-258-367-21

Query Match

Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1762 GGGAAAGCCTTTATGTCAGG 1784
111111 111111111 11111

Db 41 GGGAAAGCCTTTATGTCAGG 19

RESULT 21
US-09-546-550-21/c

; Sequence 21, Application US/09546550

; Patent No. 6284743

; GENERAL INFORMATION:

; APPLICANT: PARMACEK, MICHAEL S.

; APPLICANT: SOLWAY, JULIAN

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION

; FILE REFERENCE: ARCD:310

; CURRENT APPLICATION NUMBER: US/09/546,550

; CURRENT FILING DATE: 2000-04-10

; PRIOR APPLICATION NUMBER: 09/258,367

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 21

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; US-09-546-550-21

Query Match

Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1762 GGGAAAGCCTTTATGTCAGG 1784
111111 111111111 11111

Db 41 GGGAAAGCCTTTATGTCAGG 19

RESULT 22
US-09-431-414-21/c

; Sequence 21, Application US/09431414

; Patent No. 6291211

; GENERAL INFORMATION:

; APPLICANT: PARMACEK, MICHAEL S.

; APPLICANT: SOLWAY, JULIAN

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION

; FILE REFERENCE: ARCD:335

; CURRENT APPLICATION NUMBER: US/09/431,414

; CURRENT FILING DATE: 1999-11-01

; EARLIER APPLICATION NUMBER: 08/726,807

; EARLIER FILING DATE: 1996-10-07

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 21

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-431-414-21

Query Match 0.7%; Score 19.8; DB 4; Length 47;
Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1762 GGGAAGCCTTTATGTCAGG 1784
||||| ||||||| |||||
DB 41 GGGAAGCCTTTATGTCAGG 19

RESULT 23
US-09-225-670-21/c
Sequence 21, Application US/09225670
Patent No. 6297221
GENERAL INFORMATION:
APPLICANT: PARMACER, MICHAEL S.
APPLICANT: SOLWAY, JULIAN
TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
FILE REFERENCE: ASB:526
CURRENT APPLICATION NUMBER: US/09/225,670
CURRENT FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: 08/726,807
EARLIER FILING DATE: 1996-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-225-670-21

Query Match 0.7%; Score 19.8; DB 4; Length 47;
Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1762 GGGAAGCCTTTATGTCAGG 1784
||||| ||||||| |||||
DB 41 GGGAAGCCTTTATGTCAGG 19

RESULT 24
US-09-431-349C-21/c
Sequence 21, Application US/09431349C
Patent No. 6331527
GENERAL INFORMATION:
APPLICANT: PARMACER, MICHAEL S.
APPLICANT: SOLWAY, JULIAN
TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
FILE REFERENCE: ARSB:526
CURRENT APPLICATION NUMBER: US/09/431,349C
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/225,670
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: 08/726,807
PRIOR FILING DATE: 1996-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-431-349C-21

Query Match 0.7%; Score 19.8; DB 4; Length 47;
Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1762 GGGAAGCCTTTATGTCAGG 1784
||||| ||||||| |||||
DB 41 GGGAAGCCTTTATGTCAGG 19

RESULT 25
US-08-863-813A-47
Sequence 47, Application US/08863813A
Patent No. 6140466
GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Gottesfeld, Joel M.
APPLICANT: Wright, Peter E.
TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES
TITLE OF INVENTION: AND METHODS THEREFOR
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,813A
FILING DATE: 27-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,318
FILING DATE: 18-JUL-1996
APPLICATION NUMBER: 08/183,119
FILING DATE: 18-JAN-1996
APPLICATION NUMBER: US95/00829
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A., Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08401/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-863-813A-47

Query Match 0.7%; Score 19.8; DB 3; Length 57;
Best Local Similarity 77.4%; Pred. No. 7e+03;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1247 GGCGCACGTGGGGAAGCCTTATGCTTGC 1277
||| ||||| ||||| ||||| |||||
DB 3 GGAGGAGACCGGTGAGAGCCCTATGCTTGC 33

RESULT 26
US-09-037-990B-60/c
Sequence 60, Application US/09037990B
Patent No. 6248519
GENERAL INFORMATION:
APPLICANT: ENGEL, Stacia R.

DESCENZO, Richard A.
MORENZONI, Richard A.
IRELAN, Nancy A.
TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED MICROORGANISMS
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,990B
FILING DATE: 11-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 29520/30001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-037-990B-60

Query Match 0.7%; Score 19.8; DB 4; Length 59;
Best Local Similarity 63.8%; Pred.No.7.1e+03;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1194 AAGAAATGTGGCAGAGCTTGAAGTCAAACTCATTTACCCA 1240
DB 53 AAAAAATGTGTAGACCTTGGCGAGTAAAGCAGGCTCACCACCA 7

RESULT 27
US-08-461-184-9/c
Sequence 9, Application US/08461184
Patent No. 5631158
GENERAL INFORMATION:
APPLICANT: DORAI, HAIMANTI
APPLICANT: OPPERMANN, HERMANN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 07148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,184
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/143,498
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..56
OTHER INFORMATION: /note="PACISIG"
US-08-461-184-9

Query Match 0.7%; Score 19.6; DB 1; Length 56;
Best Local Similarity 73.5%; Pred.No.8e+03;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 567 GGAACACTATCCAGAGATCAACAAACAGC 600
DB 51 GGAACAGCAATCCAGAACATCAGCACCAACAGC 18

RESULT 28
US-08-463-675-9/c
Sequence 9, Application US/08463675
Patent No. 5658763
GENERAL INFORMATION:
APPLICANT: DORAI, HAIMANTI
APPLICANT: OPPERMANN, HERMANN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 07148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,675
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/143,498
FILING DATE: 25-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100


```

; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..56
; OTHER INFORMATION: /note="PACISIG"
US-08-463-675-9

Query Match      0.7%; Score 19.6; DB 1; Length 56;
Best Local Similarity 73.5%; Pred. No. 8e+03;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY      567 GGAAGACACTATCCAGAGATCAGAAACACAGC 600
      1111 11111111111111111111111111111111
DB      51 GGAAGCAGGAATCCAGACATCAGCACCACAGC 18

RESULT 29
US-08-464-589-9/C
; Sequence 9, Application US/08464589
; Patent No. 5733782
; GENERAL INFORMATION:
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: OPPERMANN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,589
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..56
; OTHER INFORMATION: /note="PACISIG"
US-08-464-589-9

Query Match      0.7%; Score 19.6; DB 1; Length 56;
Best Local Similarity 73.5%; Pred. No. 8e+03;
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```

Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY      567 GGAAGACACTATCCAGAGATCAGAAACACAGC 600
      1111 11111111111111111111111111111111
DB      51 GGAAGCAGGAATCCAGACATCAGCACCACAGC 18

RESULT 30
US-08-406-030A-8
; Sequence 8, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Hauge, Brian M.
; APPLICANT: Selden, Richard F
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT95-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-8

Query Match      0.7%; Score 19.6; DB 4; Length 60;
Best Local Similarity 66.7%; Pred. No. 8.4e+03;
```

NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:

ADDRESSEE: CURTIS, MORRIS & SAFORD, P.C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-99

Query Match 0.7%; Score 19.4; DB 2; Length 43;
Best Local Similarity 70.3%; Pred. No. 7.8e+03;
Matches 26; Conservative 0; Mismatches 11; Indels 0;

QY 2223 TGTGTGATATGATGACAGCTGACTGCTAAGTACT 2259
1 TTTGTATGTAATGATGATGACACTGACAGTAAAT 37

RESULT 34
US-09-641-638-760/c
Sequence 760, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patentl.pm
SEQ ID NO 760
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-400-217 : polymorphic base A or G
US-09-641-638-760

Query Match 0.7%; Score 19.4; DB 4; Length 47;
Best Local Similarity 61.7%; Pred. No. 8.2e+03;
Matches 29; Conservative 1; Mismatches 17; Indels 0;

QY 1460 TCACCTTAGCTGGAATCAACCTCAAAACACACACAGAGACACT 1506
47 TGACTTAGTTGAAAATGTACACAGTATTTCAGTAGAGAACTACT 1

RESULT 35
US-08-417-210A-106/c
Sequence 106, Application US/08417210A
Patent No. 5863542
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM T.
TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXYVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFORD, P.C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-106

Query Match 0.7%; Score 19.4; DB 2; Length 56;
Best Local Similarity 70.3%; Pred. No. 9.3e+03;
Matches 26; Conservative 0; Mismatches 11; Indels 0;

QY 2223 TGTGTGATATGATGACAGCTGACTGCTAAGTACT 2259
40 TTTGTATGTAATGATGATGACACTGACAGTAAAT 4

RESULT 36
US-08-973-965-1/c
Sequence 1, Application US/08973965
Patent No. 6033881
GENERAL INFORMATION:
APPLICANT: HIMMLER, Gottfried
APPLICANT: SCHLEDERER, Thomas
TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF
FILE REFERENCE: 030560-055
CURRENT APPLICATION NUMBER: US/08/973,965
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: AT A 1007/95
EARLIER FILING DATE: 1995-06-13

EARLIER APPLICATION NUMBER: PCT/AT96/00106
EARLIER FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO: 1
LENGTH: 41
TYPE: DNA
ORGANISM: synthetic construct
US-08-973-965-1

Query Match 0.7%; Score 19.2; DB 3; Length 41;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Y 1237 CCCACGAGGGCGCACTGGGAGAACCT 1268
DB 34 CCACCGAAGAGCTGCTGAGGCT 3

RESULT 37

US-08-444-818-229
Sequence 229, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANO Diagnostic and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Ailsa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110,002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "adaptor in an expression
cassette."
US-08-444-818-229

Query Match 0.7%; Score 19.2; DB 3; Length 44;
Best Local Similarity 67.5%; Pred. No. 9.2e+03;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Y 331 TGGAAATTCATCTTAAACCAAACTCATGCTCAGCT 370
DB 5 TGGGAATTCATATGAGACCTTAAGTATATCTCAGCT 44

RESULT 38
US-08-171-389-100
Sequence 100, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-directed DNA Binding
Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
P-450
US-08-171-389-100

Query Match 0.7%; Score 19.2; DB 1; Length 45;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Y 1353 TACATTTGACGAGAGCTGAGCAGGCTTAG 1384
DB 3 TAAATGACGAGGAGCTTATATAAACTTGG 34

RESULT 39
US-08-123-936-100

; Sequence 100, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,936
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
; INDIVIDUAL ISOLATE: P-450
; US-08-123-936-100
; Query Match 0.7%; Score 19.2; DB 1; Length 45;
; Best Local Similarity 75.0%; Pred. No. 9.3e+03;
; Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1353 TACATTTCAGGAGCTGTGACGAGCTTTAG 1384
DB 3 TAAATTACAGGAGCTGTATATAAACTTTGG 34

RESULT 40
US-08-475-228A-100
; Sequence 100, Application US/08475228A
; Patent No. 3869241
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: FTY, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods

; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,228A
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
; INDIVIDUAL ISOLATE: P-450
; US-08-475-228A-100
; Query Match 0.7%; Score 19.2; DB 2; Length 45;
; Best Local Similarity 75.0%; Pred. No. 9.3e+03;
; Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1353 TACATTTCAGGAGCTGTGACGAGCTTTAG 1384
DB 3 TAAATTACAGGAGCTGTATATAAACTTTGG 34

RESULT 41
US-08-482-080A-100
; Sequence 100, Application US/08482080A
; Patent No. 6010849
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: FTY, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive

```

1 CITY: Redwood City
2 STATE: CA
3 COUNTRY: USA
4 ZIP: 94063
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: PatentIn Release #1.0, Version #1.25
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/482,080A
14 FILING DATE: 07-JUN-1995
15 APPLICATION DATA:
16 APPLICATION NUMBER: US 08/171,389.
17 FILING DATE: 20-DEC-1993
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/123,936
21 FILING DATE: 17-SEP-1993
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/996,783
24 FILING DATE: 23-DEC-1992
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/723,618
28 FILING DATE: 27-JUN-1991
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 08/081,070
31 FILING DATE: 22-JUN-1993
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Brady, John F.
34 REGISTRATION NUMBER: 39,118
35 REFERENCE/DOCKET NUMBER: 4600-0175.20/619P3D1
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (650) 324-0880
38 TELEFAX: (650) 324-0960
39 INFORMATION FOR SEQ ID NO: 100:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 45 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: double
44 TOPOLOGY: linear
45 MOLECULE TYPE: DNA (genomic)
46 HYPOTHETICAL: NO
47 ORIGINAL SOURCE:
48 INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
49 INDIVIDUAL ISOLATE: P-450
50 US-08-482-080A-100
51
52 Query Match 0.7% Score 19.2; DB 3; Length 45
53 Best Local Similarity 75.0%; Pred. No. 9.3e+03;
54 Matches 24; Conservative 0; Mismatches 8; Indels
55
56 QY 1353 TACATTGACAGGAGCTGTGACGACGCTTTAG 1384
57 ||||| ||||| ||||| || |||||
58 Db 3 TAAATTACAGGAGCTGTATTAAACCTTGG 34
59
60 RESULT 42
61 US-09-354-947-100
62 Sequence 100, Application US/09354947
63 Patent No. 6384208
64
65 GENERAL INFORMATION:
66 APPLICANT: Edwards, Cynthia A.
67 APPLICANT: Cantor, Charles R.
68 APPLICANT: Andrews, Beth M.
69 APPLICANT: Turin, Lisa M.
70 APPLICANT: Fty, Kirk E.
71 TITLE OF INVENTION: Sequence-Directed DNA Binding
72 TITLE OF INVENTION: Molecules, Compositions and Methods
73 NUMBER OF SEQUENCES: 664
74 CORRESPONDENCE ADDRESS:
75 ADDRESSEE: Genelabs Technologies, Inc.
76 STREET: 505 Penobscot Drive
77 CITY: Redwood City

```

```

1 STATE: CA
2 COUNTRY: USA
3 ZIP: 94063
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: PatentIn Release #1.0, Version #1.25
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/09/354,947
12 FILING DATE:
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 08/482,080
15 FILING DATE: 07-JUN-1995
16 APPLICATION NUMBER: US 08/171,389
17 FILING DATE: 20-DEC-1993
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/123,936
20 FILING DATE: 17-SEP-1993
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/996,783
23 FILING DATE: 23-DEC-1992
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/723,618
26 FILING DATE: 27-JUN-1991
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 08/081,070
29 FILING DATE: 22-JUN-1993
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Brady, John F.
32 REGISTRATION NUMBER: 39,118
33 REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (650) 324-0880
36 TELEFAX: (650) 324-0960
37 INFORMATION FOR SEO ID NO: 100:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 45 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: double
42 TOPOLOGY: linear
43 MOLECULE TYPE: DNA (genomic)
44 HYPOTHEetical: NO
45 ORIGINAL SOURCE:
46 INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
47 INDIVIDUAL ISOLATE: P-450
48 US-09-354-947-100
49
50 Query Match 0.7%: Score 19.2; DB 4; Length 45;
51 Best Local Similarity 75.0%; Pred. No. 9.3e+03;
52 Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
53
54 QY 1353 TACATTGTCAGGAGGTGTGACCAAGCGCTTAG 1384
55 ||||| ||||| ||||| ||||| ||||| ||||| |||||
56 Db 3 TAAATTAGCAGGAGGTGTATAAAACTTTGG 34
57
58 RESULT 43
59 PCT-US93-12388-100
60 Sequence 100. Application PC/TUS9312388
61 GENERAL INFORMATION:
62 APPLICANT:
63 TITLE OF INVENTION: Sequence-Directed DNA Binding
64 TITLE OF INVENTION: Molecules, Compositions and Methods
65 NUMBER OF SEQUENCES: 641
66 CORRESPONDENCE ADDRESS:
67 ADDRESSEE: GeneLabs Technologies, Inc.
68 STREET: 505 Penobscot Drive
69 CITY: Redwood City
70 STATE: CA
71 COUNTRY: USA
72 ZIP: 94063
73
74 COMPUTER READABLE FORM:

```

RESULT 44
 US-08-859-649-10
 Sequence 10, Application US/08859649
 Patent No. 5874060
 GENERAL INFORMATION:
 APPLICANT: Armour, Kathryn L.
 APPLICANT: Carr, Francis J.
 APPLICANT: Old, Lloyd J.
 APPLICANT: Kitamura, Kunio
 APPLICANT: Garin-Chesa, Pilar
 TITLE OF INVENTION: Recombinant Human Anti-Lewis Y
 TITLE OF INVENTION: Antibodies
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 2730 Sand Hill Road
 CITY: Menlo Park
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/859,649
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

```
US-08-207-861-10  
SEQUENCE 10, APPLICATION US/08207861  
PATENT NO. 6310185  
GENERAL INFORMATION:  
APPLICANT: Armour, Kathryn L.  
INVENTOR: Carr, Francis J.  
APPlicant: Old, Lloyd J.  
APPlicant: Kitamura, Kunio  
APPlicant: Garin-chesa, Pilar  
TITLE OF INVENTION: Recombinant Human Anti-Lewisx  
TITLE OF INVENTION: Antibodies  
NUMBER OF SEQUENCES: .33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 2730 Sand Hill Road  
CITY: Menlo Park  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/207,861  
FILING DATE: 08-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 7606-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEx: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA  
US-08-207-861-10
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Query Match 0.7%; Score 19.2; DB 4; Length 48;
Best Local Similarity 67.5%; Pred. No. 9.7e+03;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 472 TTTTCTCCAGTCAGAGCTTCACCCACATGTGTGGCT 511
Db 1 TTGGCCCGAGTAAGCAACACGACGACCATACGGGTGCT 40

RESULT 46

US-08-431-527A-6
Sequence 6, Application US/08431527A
Patent No. 5843650
GENERAL INFORMATION:
APPLICANT: David Segev
TITLE OF INVENTION: No. 5843650-enzymatic method for detecting nucleic acid sequen
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Robert Shelnbein
STREET: 2940 Birchtree space lane
CITY: Silver Spring
STATE: Maryland
COUNTRY: United States of America
ZIP: 20906
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,527A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 128/8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6938541
TELEFAX: 972-3-6938542
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-431-527A-6

Query Match 0.7%; Score 19.2; DB 2; Length 58;
Best Local Similarity 62.5%; Pred. No. 1.1e+04;
Matches 30; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 73 TACCTGATTCGGCTTCAGATCCGCGCTGCACCCGCGTTCATC 120
Db 1 TACATGTGTACAGTTCTCTGCATGGCGCATGAACCGAGGCCCATC 48

RESULT 47

US-08-485-355B-53
Sequence 53, Application US/08485355B
Patent No. 6177075
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
TITLE OF INVENTION: Insect Viruses and Their Uses in
Protecting Plants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Tregerlin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: DNA
MOLECULE TYPE: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-08-485-355B-53

Query Match 0.7%; Score 19.2; DB 4; Length 59;
Best Local Similarity 62.5%; Pred. No. 1.1e+04;
Matches 30; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 759 GTGATATAGGGTCCAGCCCTGAAGCGGAGCATCTAGAGGAACA 806
Db 1 GGGATCCACAGTTCTGCTCCCGGAGCGTAATATAGGGGAACA 48

RESULT 48

US-08-373-124A-185/C
Sequence 185, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Slinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-185

Query Match 0.7% Score 19: DB 1: Length 38;
Best Local Similarity 71.4% Pred. No. 9.6e+03;
Matches 25: Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 35 CTCCTCTTAAGTCTTCCACACCTGCTCT 69
Db 38 CTCCTCTTTCGGCTTCGGCTCATCAGCTCT 4

RESULT 49
US-08-435-628-185/c
Sequence 185, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124

FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-185

Query Match 0.7% Score 19: DB 1: Length 38;
Best Local Similarity 71.4% Pred. No. 9.6e+03;
Matches 25: Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 35 CTCCTCTTAAGTCTTCCACACCTGCTCT 69
Db 38 CTCCTCTTTCGGCTTCGGCTCATCAGCTCT 4

RESULT 50
US-09-609-816-13
Sequence 13, Application US/09609816
Patent No. 6436684
GENERAL INFORMATION:
APPLICANT: Woodage, Trevor
APPLICANT: Wei, Minh Hui
APPLICANT: Kodira, Chinappa
APPLICANT: Beasley, Ellen
APPLICANT: DiFrancesco, Valentina
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
FILE REFERENCE: CLO00669PCT
CURRENT APPLICATION NUMBER: US/09/609,816
CURRENT FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/192,408
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/212,725
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/609,816
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
TYPE: DNA
LENGTH: 46
ORGANISM: HUMAN
US-09-609-816-13

Query Match 0.7% Score 19: DB 4: Length 46;
Best Local Similarity 62.2% Pred. No. 1.1e+04;
Matches 28: Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 2708 CATCCCTCTTCACGACGCTGTTTGGTCAATAAATCT 2752
Db 2 CAACCCCTCTTCCTGTAACCTTAATCTCTTAACCACTCT 46

Fri Jun 6 11:21:42 2003

us-09-898-556a-3.szlm60.mri

Page 24

Search completed: June 4, 2003, 10:26:12
Job time : 167 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 06:49:48 ; Search time 3825 Seconds
(without alignments)
11736.965 Million cell updates/sec

Title: US-09-898-556A-3

Perfect score: 2772

Sequence: 1 cagcgcgcttaagctggtg.....ttctaccatccacacct 2772

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 146654

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estcpl:*
7: em_estro:*
8: em_estl:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	34	1.2	60	AA834171	AA834171 o114e11.s
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C 4	28.2	1.0	52	AA425976	AA425976 zw1b06.r
C 5	27.6	1.0	58	AA994682	AA994682 ou58c08.s
C 6	26.6	1.0	58	AI597270	AI597270 v154d09.x

7	26.4	1.0	46	AA902889	AA902889 o149g04.s
C 8	25.8	0.9	55	AA136306	AA136306 zn89c02.s
C 9	24.6	0.9	45	A2513479	A2513479 1m0359p21
C 10	24.4	0.9	50	AA948106	AA948106 on51a04.s
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C 13	23.6	0.9	46	AA867748	AA867748 vx16a12.r
C 14	23.4	0.8	49	AA227017	AA227017 z1r1c09.r
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C 16	22.8	0.8	37	1783009	1783009 y439a12.r11
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C 20	22.6	0.8	55	B1963825	B1963825 i6e5a07.x
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C 23	22.2	0.8	43	AA227334	AA227334 z1r1b11.r
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C 252	18.2	0.7	50	17	AZ313593	AZ313593 1M030B05	C 325	18	0.6	56	14	F35060	F35060 HSPD30590 H
C 253	18.2	0.7	51	17	CNS02VIL	AL215814	C 326	18	0.6	56	17	A2962794	A2962794 2M0231D15
C 254	18.2	0.7	52	9	AA869327	AA869327 vq50f08.r	C 327	18	0.6	56	17	HSMC09F1	HSMC09F1
C 255	18.2	0.7	52	9	AA888532	AA888532 nw81a04.s	C 328	18	0.6	57	17	AI930814	AI930814
C 256	18.2	0.7	52	9	AI154969	AI154969 ud82b10.r	C 329	18	0.6	57	13	B1714149	B1714149
C 257	18.2	0.7	52	9	AI970313	AI970313 wr09e04.x	C 330	18	0.6	57	17	TA348B10P	TA348B10P
C 258	18.2	0.7	52	9	AA511416	AA511416 vj72e10.r	C 331	18	0.6	58	9	AA489706	AA489706
C 259	18.2	0.7	52	10	BE042312	BE042312 hk35d07.Y	C 332	18	0.6	58	9	BU077758	BU077758
C 260	18.2	0.7	52	17	AZ437199	AZ437199 1M0067J09	C 333	18	0.6	58	13	BM434781	BM434781
C 261	18.2	0.7	52	17	AZ447457	IM0244E08	C 334	18	0.6	58	13	AZ320565	AZ320565
C 262	18.2	0.7	53	17	AZ484807	IM0311J02	C 335	18	0.6	58	17	AZ789611	AZ789611
C 263	18.2	0.7	53	17	CNS01SD9	AL165078	C 336	18	0.6	58	17	CNS0220S	CNS0220S
C 264	18.2	0.7	54	10	AM590712	h48a02.x	C 337	18	0.6	58	17	AA734809	AA734809
C 265	18.2	0.7	54	10	AZ944165	2M0205B08	C 338	18	0.6	59	9	AU255513	AU255513
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C 267	18.2	0.7	55	14	R93606	R93606 yq34c12.s1	C 340	18	0.6	59	13	AZ774339	AZ774339
C 268	18.2	0.7	55	14	AZ983943	AZ983943 2M0256G18	C 341	18	0.6	59	17	BE324712	BE324712
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C 293	18.2	0.7	59	10	AA071902	AA071902 2M0112B03	C 366	18	0.6	60	17	AZ933796	AZ933796
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C 375	17.8	0.6	50	9	AU107309	AU107309	C 448	17.6	0.6	49	9	A1865173	A1865173	vk09b01.x
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C 393	17.8	0.6	55	14	H51371	H51371	C 466	17.6	0.6	52	9	AA914838	AA914838	
C 394	17.8	0.6	55	17	AH3377	AH3377	C 467	17.6	0.6	52	9	A1799301	A1799301	
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C 397	17.8	0.6	55	17	TA170H10Q	TA170H10Q	C 470	17.6	0.6	53	17	A2789268	A2789268	
C 398	17.8	0.6	56	14	FA34759	FA34759	C 471	17.6	0.6	53	17	A2789268	A2789268	
C 399	17.8	0.6	56	17	AZ328238	AZ328238	C 472	17.6	0.6	53	17	AZ805887	AZ805887	
C 400	17.8	0.6	57	9	AA911978	AA911978	C 473	17.6	0.6	54	17	AA790169	AA790169	
C 401	17.8	0.6	57	9	AZ618308	AZ618308	C 474	17.6	0.6	54	17	AZ435796	AZ435796	
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C 403	17.8	0.6	57	17	BH758527	BH758527	C 476	17.6	0.6	55	9	AA146706	AA146706	
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C 420	17.6	0.6	62	9	AU258235	AU258235	C 493	17.6	0.6	58	9	AA889400	AA889400	
C 421	17.6	0.6	62	9	AU012250	AU012250	C 494	17.6	0.6	58	9	AA889400	AA889400	
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RESULT 1	AA757305/c	58 bp	linear	EST 31-DEC-1998
LOCUS	AA757305			
DEFINITION	ab96609.s1 Soares_NFL_T-GBC_S1 Homo sapiens CDNA clone IMAGE:1326952 3' similar to gb:X07290_cds1 ZINC FINGER PROTEIN			
ACCESSION	AA757305			
VERSION	AA757305.1			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Eumetazoa; Mammalia; Primates; Hominidae; Homininae; Homo			

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AA757305/c
 58 bp mRNA linear EST 31-DEC-1998
 IMAGE:1326952 3 similar to gb:X07290.cdsl ZINC FINGER PROTEIN
 IMAGE:1326952 3 similar to gb:X07290.cdsl ZINC FINGER PROTEIN

AA757305
 AA757305.1 GI:2805168
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	Mammalia: Eutheria; Primates; Catarrhini; Hominoidea: Homo.
AUTHORS	1 (bases 1 to 58)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
COMMENT	Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.

FEATURES	source
<p> Contact: Robert Strassberg, Ph.D. Email: cgabbs-r@email.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality Insert Length: 669 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1..36 </p>	

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1326952"
/clone_lib="Soares_NFL_T-GBC-S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung Nblh19W, testis NHT, and B-cell
NCLCGAP-GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The drive
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1.M.A.G.-E. .C.M.A.S. 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

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Query Match	1.2%	Score 34	DB 9	Length 58
Best Local Similarity	80.0%	Pred. No. 38		
Matches 40; Conservative	0	Mismatches 10	Indels 0	Gaps 0

QY 1071 CATCAGAGGACACACTCTCAGGGGAGAAACCTTATGTCGCAAGCATTTGTGG 1120
||||||| | ||| | ||||||||| | ||||| |||||
Db 58 CATCAGAGATTTCACACTGGTGAGAAACCTTATGCATGTAAGCATGTGG 9

RESULT 2	AA834171/c	LOCUS	DEFINITION
	AA834171	60 bp	mRNA
	of:cell.1.s1	NCI CGAP Kid6	Homo sapiens
		CGNA clone	IMAGE:1421132
		similar to gp.X16282_cds1	ZINC FINGER PROTEIN CLONE 647 (HUMAN);
		mRNA sequence:	

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VERSION      AA834171.1  GI:2907770
KEYWORDS
SOURCE       EST.
              human.

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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 60)	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap .		
	National Cancer Institute,	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.			

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rtiemail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/MLND at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCICGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/HLNt at: www-bio.linn.gov/bdip/image/image.html

FEATURES

Trace considered overall poor quality

Insert Length: 2306 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/qualifiers

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/db_xref="taxon:9606"
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/sex="mixed"
/tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site:1:
ECORI; Site:2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3'. Average insert size: 1.0 kb."
BASE COUNT
ORIGIN
7 a 19 c 14 g 20 t

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Query Match	1.2%	Score 34	DB 9	Length 60
Best Local Similarity	80.0%	Pred. No. 39		
Matches 40; Conservative	0	Mismatches 10	Indels 0	Gaps 0

QY 1322 ACACAGAGGACACATTCAGGAGAGAACCCTTACATTTCAGGGAGCTGTG 1371

Db 59 AGACAAGAGGATCCACACAGGAGAGACGCCCTTACAGTGCGACGGAGCTGTG 10

RESULT 3	AA864103	LOCUS	DEFINITION
AA864103	58 bp	mouse mRNA	linear EST 11-MAR-1998
AA864103	58 bp	Stratagene mouse strain (#937313)	Mus musculus cDNA clone
AA864103	58 bp	IMAGE:1023866	5' similar to gb:U10632 mouse mRNA for zinc finger protein (MOUSE);, mRNA sequence.

ACCESSION	AA864103	
VERSION	AA864103.1	GI:29565822
KEYWORDS	EST.	
SOURCE	house mouse,	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eumetazoa: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 58)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The MASHU-HMMT Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST project

WashU-NHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
TEL: 314 286 1800
FAX: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:574642
Seq primer: -28m13 rev1 ET from Amersham

FEATURES High quality sequence stop: 1.
Location/Qualifiers

1..58
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1023866"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' GAATTCGCGCAGCAG 3' -3' adaptor
sequence: 5' CTCGACTTTTCTTTTCTTTT 3'"

BASE COUNT 20 a 9 c 15 g 14 t

ORIGIN

Query Match 1.0%; Score 28.4; DB 9; Length 58;
Best Local Similarity 70.4%; Pred. No. 1.9e+03;
Matches 38; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1330 GGACACATTCAGAGAGAGCCTTACATTCGACGAGGTGTAGCAAGGCTTTA 1383
DB 5 GGAATTATACAGTGTAGCAAGCCTTACAAATCGGTGTAATGTGCAAAATCCTTA 58

RESULT 4
LOCUS AA425976 52 bp mRNA linear EST 16-OCT-1997
DEFINITION zw17b06.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone
IMAGE:769523 5' similar to TR:G340458 G340458 DNA-BINDING PROTEIN
; mRNA sequence.
AA425976
AA425976.1 GI:2107852
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 52)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gaisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
T., Waterston, R., and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
SOURCE
1..52
/organism="Homo sapiens"
/db_xref="GDB:5979393"
/db_xref="taxon:9606"
/clone="IMAGE:769523"
/clone_lib="Soares ovary tumor NBHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCGTACCAATTCAGAGTGTAGGAGCGCGGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo.

BASE COUNT 16 a 10 c 15 g 11 t

ORIGIN

Query Match 1.0%; Score 28.2; DB 9; Length 52;
Best Local Similarity 73.5%; Pred. No. 2e+03;
Matches 36; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1661 CCAGAGGACACATTCAGGAGGAGACCATTTGTATGCTGAGTGTGCA 1709
DB 1 CCAGAGATTCACACAGGAGGAGACCATTCCTGTATGTGTGTGCA 49

RESULT 5
LOCUS AA994682/C 58 bp mRNA linear EST 03-JUN-1998
DEFINITION ou58c08.s1 NCI-CGAP Br2 Homo sapiens cDNA clone IMAGE:1632014 3'
similar to TR:O14899 O14899 ZINC FINGER PROTEIN ; mRNA sequence.
AA994682
AA994682.1 GI:3181171
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 58)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html

JOURNAL
COMMENT
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
SOURCE
1..58
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1632014"
/clone_lib="NCI CGAP Br2"
/sex="Female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. This library is the normalized version of
NCI-CGAP Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo.

BASE COUNT 10 a 16 c 18 g 14 t

ORIGIN

Query Match 1.0%; Score 27.6; DB 9; Length 58;

Best Local Similarity 67.2%; Pred. No. 3.3e+03;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1491 CACGAGACACATTCAGGGGTTAAACCTTATGTCCTCGGATGGGGAGNGCT 1548
||||| 11 ||||| 1111 ||||| 1111 ||||| 111111
Db 58 CACCTGTATACGACTCGGGGAGAAACCTTCAAGTCCCGAGTCCGCAAGTGT 1

RESULT 6
AI597270/c

LOCUS 58 bp mRNA linear EST 21-APR-1999
DEFINITION vi44d09.x1 Beddington mouse embryonic region Mus musculus cDNA
clone IMAGE:907601 3' similar to gb:x74855 M.musculus zfp-51 mRNA
for a zinc finger protein (MOUSE);, mRNA sequence.

ACCESSION AI597270
VERSION AI597270.1 GI:4606318

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, T., Person
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritzer
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
Unpublished (1999)

CONTACT: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:528265

This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: polyT not found
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 1.

FEATURES

source

1. 58
/organism="Mus musculus"
/strain="C57BL/6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:907601"
/clone_lib="Beddington mouse embryonic region"
/sex="pooled"
/tissue_type="embryo"
/dev_stage="7.5dpc"
/lab_host="DH12S"

/note="Organ: Whole embryo; Vector: pCMV-SPORT; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Gastrulating embryos were collected at 7.5dpc
from C57BL/6 x DBA matings, excluding embryos that had
developed head folds and all extraembryonic tissues.
Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
Referenced in Development 121, 2479-2489 (1995)."

BASE COUNT

17 a 11 c 10 g 20 t

ORIGIN

Query Match 1.0%; Score 26.6; DB 9; Length 58;
Best Local Similarity 66.7%; Pred. No. 6.7e+03;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1746 CAGAGACACATTCAGGGGAAAGCCTTTATGTCGAGGAGTGGCAGAGATT 1802
||||| 11 ||||| 1111 ||||| 1111 ||||| 111111
Db 57 CAGAGATTTCATTCGAGAGAAACCTTCCAAAGTAAGATGATGCGCAATCTTT 1

RESULT 7
AA902889

LOCUS 46 bp mRNA linear EST 09-JUN-1998
DEFINITION o149g04.s1 NCI-CGAP_Kid3 Homo sapiens cDNA clone IMAGE:150186 3'
similar to TR:Q29294 Q29294 ZINC FINGER PROTEIN; , mRNA sequence.

ACCESSION AA902889
VERSION AA902889.1 GI:3038012

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bhrp/image/image.html

Trace considered overall poor quality
Insert Length: 1180 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source

1. 46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:150186"
/clone_lib="NCI-CGAP_Kid3"
/lab_host="DH10B"

/note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. mRNA
source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo."

BASE COUNT

11 a 19 c 13 g 3 t

ORIGIN

Query Match 1.0%; Score 26.4; DB 9; Length 46;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1560 TCAACCTTAACACACAGAGGTCACACAGCGGGGAGAACCC 1603
||||| 11 ||||| 1111 ||||| 1111 ||||| 111111

Db 2 TCGGACCTCACCACAGCAGCGCGCACGACAGCGGCGAGAGCC 45

RESULT 8
AA136306/c

LOCUS 55 bp mRNA linear EST 30-NOV-1996
DEFINITION zn89c02.s1 Stragelene lung carcinoma 937218 Homo sapiens cDNA clone
IMAGE:565346 3' similar to SW:KR4_HUMAN P10075 HKR4 PROTEIN; , mRNA
sequence.

ACCESSION AA136306
VERSION AA136306.1 GI:1697533

KEYWORDS
SOURCE

ORGANISM

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

REFERENCE 1 (bases 1 to 55)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Duboue, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucada, T., Lacy, M., Le, M., Le, N., Marlis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Treaskis, L.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
TITLE Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible conserved clone: similarity on wrong strand
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 1.
FEATURES
Source
1..55
/organism="Homo sapiens"
/db_xref="GD8:4594411"
/db_xref="taxon:9606"
/clone="IMAGE:565346"
/clone_1lb="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: lung; Vector: pBluescript SK-; Site: 1: ECORI
Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Small cell carcinoma cell line NCI-H69. Average
insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor
sequence: 5' GAATTCGGCAGCAGC 3' -3' adaptor sequence: 5'
CTCGACCTTTTCTTTTCTTTTCTTTT 3'"
BASE COUNT 11 a 12 c 11 g 11 t 10 others
ORIGIN
Query Match 0.9%; Score 25.8; DB 9; Length 55;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1050 TGGAGCTCAACCTGCATCAGACAGCAGCAGGAGGAGAACTTATG 1104
111 111 111 111 111 111 111 111 111 111 111 111
55 TGGCCTCTCATCTGNNNAGCATNAGANNNTTCACTCAGGAGGAAACCCNTATG 1
111 111 111 111 111 111 111 111 111 111 111 111
RESULT 9
LOCUS A2513479 45 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0359P21R Mouse 10kb plasmid UUGC1M library Mus musculus genom.c
ACCESSION A2513479
VERSION A2513479.1 GI:10694795
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

```

```

REFERENCE 1 (bases 1 to 55)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Duboue, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucada, T., Lacy, M., Le, M., Le, N., Marlis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Treaskis, L.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
TITLE Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible conserved clone: similarity on wrong strand
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 1.
FEATURES
Source
1..55
/organism="Homo sapiens"
/db_xref="GD8:4594411"
/db_xref="taxon:9606"
/clone="IMAGE:565346"
/clone_1lb="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: lung; Vector: pBluescript SK-; Site: 1: ECORI
Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Small cell carcinoma cell line NCI-H69. Average
insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor
sequence: 5' GAATTCGGCAGCAGC 3' -3' adaptor sequence: 5'
CTCGACCTTTTCTTTTCTTTTCTTTT 3'"
BASE COUNT 11 a 12 c 11 g 11 t 10 others
ORIGIN
Query Match 0.9%; Score 25.8; DB 9; Length 55;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1050 TGGAGCTCAACCTGCATCAGACAGCAGCAGGAGGAGAACTTATG 1104
111 111 111 111 111 111 111 111 111 111 111 111
55 TGGCCTCTCATCTGNNNAGCATNAGANNNTTCACTCAGGAGGAAACCCNTATG 1
111 111 111 111 111 111 111 111 111 111 111 111
RESULT 10
LOCUS AA948106/c 50 bp mRNA linear EST 23-JUN-1998
DEFINITION on51a04.s1 NCI-CGAP C08 Homo sapiens cDNA clone IMAGE:1560174 3'
similar to gb:M58297 ZINC FINGER PROTEIN 42 (HUMAN);. mRNA
sequence.
ACCESSION AA948106
VERSION AA948106.1 GI:3109359
KEYWORDS EST.
SOURCE human.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.

```

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbtp/image/image.html

Trace considered overall poor quality
 Insert Length: 1844 Std Error: 0.00
 Seq primer: -40m13 fwd. Err from Amersham
 High quality sequence stop: 1.

FEATURES

Source

Location/Qualifiers

1. .50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1560174"
 /clone_lib="NCI_CGAP_C08"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 colon adenocarcinoma, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bernaldo."
 BASE COUNT 5 a 15 c 21 g 9 t
 ORIGIN

Query Match 0.9%; Score 24.4; DB 9; Length 50;
 Best Local Similarity 68.0%; Pred. No. 2.8e+04;
 Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1658 GCACCAGGACACCTCAGGGAGAGACCATTTTGTCTGCTGCTG 1707
 Db 50 GCACCAGGACATCCACGAGGAGAGACCATTTTGTCTGCTGCTG 1

RESULT 11 38 bp mRNA linear EST 04-MAY-1995
 R37288 yf67a06.s1 Soares infant brain INIB Homo sapiens CDNA clone
 LOCUS IMAGE:27044 3' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE
 DEFINITION 647 (HUMAN); mRNA sequence.

ACCESSION R37288
 VERSION R37288
 KEYWORDS EST.
 SOURCE R37288.1 GI:794744

ORGANISM Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 38)

REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
 R., Williamson, A., Wohldmann, P. and Wilson, R.
 The Mashu-Merck EST Project
 Unpublished (1995)

TITLE The Mashu-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Insert Size: 690
 High quality sequence starts: 1 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL This clone is available royalty-free
 through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
 for further information. Trace considered overall poor quality
 Insert Length: 690 Std Error: 0.00
 Seg primer: -21m13
 High quality sequence stop: 1.
 Location/Qualifiers

source

1. .38
 /organism="Homo sapiens"
 /db_xref="GDB:399391"
 /db_xref="taxon:9606"
 /clone="IMAGE:27044"
 /clone_lib="Soares infant brain INIB"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: Lactid BA; Site 1: Not
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(dT) primer 15'
 AACTGGAAGAAATTCGCGCCGACAGATTATTTTATTTTATTTT 3';
 double-stranded cDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the Lactid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bernaldo."
 BASE COUNT 10 a 12 c 5 g 10 t
 ORIGIN

Query Match 0.9%; Score 23.8; DB 14; Length 38;
 Best Local Similarity 77.8%; Pred. No. 3.5e+04;
 Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1179 AAGCCTATGTGTCAGAGATGCGGACGCTT 1214
 Db 36 AAGCCTATGAGTGTATGATGATGAGGAGCCTT 1

RESULT 12 59 bp mRNA linear EST 12-SEP-2001
 B1650525 603296501f1 NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5337481 5,
 LOCUS B1650525
 DEFINITION mRNA sequence.
 ACCESSION B1650525
 VERSION B1650525.1 GI:15564761

KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 59)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Lotmar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM11857 row: a column: 02
 High quality sequence stop: 57.

TITLE High quality sequence stop: 57.
 JOURNAL
 COMMENT
 Location/Qualifiers

1. .59
 /organism="Mus musculus"
 /strain="129,C57BL/6J,FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5337481"
 /clone_lib="NCI_CGAP_Mam3"
 /tissue_type="tumor, gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lotmar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

BASE COUNT	13 a	13 c	23 g	10 t
ORIGIN				
Query Match	0.9%; Score 23.8; DB 13; Length 59;			
Best Local Similarity	72.1%; Pred. No. 4.7e+04;			
Matches	31; Conservative	0; Mismatches	12; Indels	0; Gaps
Db	699 GCACCTTCCAGCCCACTGTGAACACACAGCCACGACGACTCA 741			
	11 11 111111 111 1111 11111 11 1111 11			
	54 GCTGCTTCAGCCCGCCCTCAAGACTGACAGCCCTGGCGGACTTCA 12			
RESULT 13				
LOCUS	AA867748			
DEFINITION	AA867748 46 bp mRNA linear EST 16-MAR-1996			
	vxi2a1.r1 Soares_thymus_2bmt Mus musculus cDNA clone			
	IMAGE:1264606 5' similar to SW:2154_HUMAN Q13106 ZINC FINGER			
ACCESSION	AA867748			
VERSION	AA867748.1 GI:2963193			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 46)			
AUTHORS	Marra,N., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,I.,			
	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,			
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,			
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R., and			
	Waterson,R.			
TITLE	The WashU-HHMI Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	Contact: Marra M/Mouse EST Project			
	WashU-HHMI Mouse EST Project			
	Washington University School of Medicine			
	444 Forest Park Parkway, Box 8501, St. Louis, MO 63108			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: mouseest@watson.wustl.edu			
	This clone is available royalty-free through LLNL; contact the			
	IMAGE Consortium (info@image.llnl.gov) for further information.			
	MGI:667158			
	Trace considered overall poor quality			
	Possible reversed clone; similarity on wrong strand			
	Seq primer: -28m13 rev2 ET from Amersham			
	High quality sequence stop: 1.			
FEATURES				
source	1. 46			
	/organism="Mus musculus"			
	/strain="C57BL/6J"			
	/db_xref="taxon:10090"			
	/clone="IMAGE:1264606"			
	/clone_lib="Soares_thymus_2bmt"			
	/sex="male"			
	/tissue_type="thymus"			
	/dev_stage="4 weeks"			
	/lab_host="DH10B"			
	/note="Vector: pT73D-Pac (Pharmacia) with a modified			
	polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA			
	was primed with a Not I - oligo(dT) primer [5',			
	TGTTACCAATCTCAAGTGGAGCGCGCGCTTTTCTTTTCTTTTCTTTTCTTTT			
	3']; double-stranded cDNA was ligated to Eco RI adaptors			
	(Pharmacia), digested with Not I and cloned into the Not I			
	and Eco RI sites of the modified pT73 vector. RNA			
	provided by Dr. Bertrand Jordan. Library went through two			
	rounds of normalization, and was constructed by Bento			
	Soares and M.Paloma Bonaldo."			
BASE COUNT	11 a	11 c	15 g	9 t
ORIGIN				
Query Match	0.9%; Score 23.6; DB 9; Length 46;			
Best Local Similarity	69.6%; Pred. No. 4.6e+04;			

Matches	32: Conservative	0: Mismatches	14: Indels	0: Gaps
QY	1760	ACGGGAAAAGCCTTTTATGTCGAGGAGCTGTGGCAGAAAGCTTCCG	1805	
Db	1	ACGTGACAAAGCCACCAAGTGTCTGATGTGGCAAAAGCTTCCG	46	
RESULT 14				
LOCUS	AA227017			
DEFINITION	AA227017	49 bp	mRNA	linear
ACCESSION	AA227017			EST 11-MAR-1996
VERSION	AA227017.1	GI:1848638		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases 1 to 49)			
AUTHORS	Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Maria,M., Martin,J., Moore,B., Schellenberg,K., Stepec,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.			
TITLE	WashU-NCI human EST Project			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1628 Std Error: 0.00 Seq primer: -28m13 rev1 ER from Amersham High quality sequence stop: 40. Location/Qualifiers 1. 49 /organism="Homo sapiens" /db_xref="GDB:5589788" /db_xref="taxon:9606" /clone="IMAGE:663856" /clone_id="Stratagene NT2 neuronal precursor 937230" /tissue_type="neuroepithelial cells" /dev_stage="Ntera-2 neuroepithelial cells" /lab_host="SOLR (kanamycin resistant)" /note="Organ: brain; Vector: pBluescript SK-; Site:1; EcoRI; Site:2; XhoI; Cloned unidirectionally. Primer: Oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/Cl.D1). Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGACTTTTTTTTTTTTTTT 3'."			
FEATURES				
SOURCE				
BASE COUNT	20 a	9 c	9 g	11 t
ORIGIN				
Query Match	0.8%;	Score 23.4;	DB 9;	Length 49;
Best Local Similarity	67.3%;	Pred. No. 5.5e+04;		
Matches	33;	Conservative 0;	Mismatches 16;	Indels 0;
			Gaps 0;	
QY	1052	GAAGTCAACCTGATCACACATCAGAGGACACTCGGGGAGAAACCT	1100	
Db	1	GAATAGAAAGTCTATTGACATCAGAAATTCACACATGCGAGAAACCT	49	
RESULT 15				
LOCUS	BF638864			
DEFINITION	BF638864	60 bp	mRNA	linear
ACCESSION	BF638864			EST 19-DEC-2000
VERSION	BF638864.1	GI:11903022		

BASE COUNT	16 a	22 c	9 g	8 t	1 others
ORIGIN					


```

RESULT 22
AL757225/c 60 bp DNA linear GSS 18-JUN-2002
LOCUS AL757225
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-119G01-012822,
ACCESSION AL757225
VERSION AL757225.1 GI:21495573
KEYWORDS GSS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weissshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
JOURNAL Unpublished
REFERENCE
2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE
3 Strizhov,N., Rosso,M., Li,Y. and Weissshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the right border of the T-DNA. It
indicates an insertion within the locus defined by clone F19K16.
The sequences are generated at the MPI for Plant Breeding Research
in the context of the GABI-Kat project. GABI-Kat is part of the
German Plant Genomics program designated 'GABI'. Information on
line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
location/Qualifiers
1. 60
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-119G01-012822"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
BASE COUNT 27 a 14 c 9 g 10 t
ORIGIN
Query Match 0.8%; Score 22.6; DB 17; Length 60;
Best Local Similarity 75.7%; Pred. No. 1.1e+05;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 2468 AACCTGCTTCCCATTTGCTGCTTCCCTCCGATG 2504
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 42 AACATGTCATTCATGTCGTCCTTCTTTATG 6

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RESULT 23
AA227334 43 bp mRNA linear EST 11-MAR-1998
LOCUS AA227334
DEFINITION zrl7b1l.1 Stralagene NT2 neuronal precursor 937230 Homo sapiens
CNA clone IMAGE:663645 5' similar to TR:G1049295 G1049295 KRAE
ZINC FINGER PROTEIN ;, mRNA sequence.
ACCESSION AA227334
VERSION AA227334.1 GI:1848937

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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 43)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisler,G., Jost,S.,
Krisman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,
J., Moore,B., Schellenberg,K., Stepien,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
MasNU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert length: 1843 Std Error: 0.00
Seq primer: -28m3 rev1 ET from Amersham
High quality sequence stop: 1.
FEATURES
source
location/Qualifiers
1. 43
/organism="Homo sapiens"
/db_xref="GDB:558575"
/db_xref="taxon:9606"
/clone="IMAGE:663645"
/clone_lib="Stralagene NT2 neuronal precursor 937230"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/note="organ: brain; Vector: pBluescript SK-; Site:1:
EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
Oligo: dt. Uninduced, exponentially growing neuroepithelial
cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCGCGAG
3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"
BASE COUNT 7 a 8 c 15 g 13 t
ORIGIN
Query Match 0.8%; Score 22.2; DB 9; Length 43;
Best Local Similarity 69.8%; Pred. No. 1.2e+05;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 206 GCGCTTCGTCGATTCAGGATGCGCTGACTTACCCAG 248
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GCATTCAGTCAGCTTCATGATGTCGTCGAGTCCCGAG 43

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RESULT 24
BM566527 52 bp mRNA linear EST 20-FEB-2002
LOCUS BM566527
DEFINITION k163e09.y1 Ascaris suum male gut SL1 TOPO v1 Murphy Chippelli
ACCESSION BM566527
VERSION BM566527.1 GI:18827611
KEYWORDS EST.
SOURCE pig roundworm.
ORGANISM Ascaris suum
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea
; Ascarididae; Ascaris.
REFERENCE
1 (bases 1 to 52)
McCarter,J., Clifton,S., Chiappelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Rittler,E., Bennett,J., Franklin,C., Tsagarishevili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,
M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
TITLE

```


JOURNAL COMMENT

Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
The library was constructed by Claire Murphy, Brandi Chiappelli, and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center.

FEATURES

Source

1..52

/organism="Ascaris suum"

/db_xref="taxon:6253"

/clone_lib="Ascaris suum male gut SL1 TOPO v1 Murphy Chiappelli McCarter"

/sex="Male"

/tissue_type="Intestine"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Vector: pCRIT-TOPO (Invitrogen); Site_1: EcoRI; Site_2: EcoRI. The library was constructed by Claire Murphy, Brandi Chiappelli, and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Ascaris suum male intestine cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRIT-TOPO(Invitrogen) following the TOPO TA cloning protocol. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhsph.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD"

BASE COUNT 15 a 9 c 16 g 12 t
ORIGIN

Query Match 0.8%; Score 22.2; DB 13; Length 52;
Best Local Similarity 69.8%; Pred. No. 1.3e+05;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1643 ATCAACCTGATCAGCAGACAGACACTCAGGAGGAG 1685
DB 7 ATCAACGCTGCTCATGTAAGAAGAGACAGATTCCAGTCAGAGAG 49

RESULT 25

AZ310125/c

LOCUS 48 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0018M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0018M20 R, DNA sequence.

ACCESSION

AZ310125

AZ310125.1 GI:10351801

VERSION

KEYWORDS

GSS.

SOURCE

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

REFERENCE

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

FEATURES

Source

1..48

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0018M20"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (9147321141gbl/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 19 c 16 g 10 t
ORIGIN

Query Match 0.8%; Score 22; DB 17; Length 48;
Best Local Similarity 67.4%; Pred. No. 1.4e+05;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 162 GAGACCAGGAATGCTACAGGCTCCTGAGAGCCAAAAGAGG 207
DB 46 GGGACTGGGCGCAGTGCTACAGCGCCGCCGCCACAGAGAGG 1

RESULT 26

AZ665324/c

LOCUS 55 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0546007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0546007 R, DNA sequence.

ACCESSION

AZ665324

AZ665324.1 GI:11802470

VERSION

KEYWORDS

GSS.

SOURCE

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 55)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

REFERENCE

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)⁺ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M. Fatima Bonaldi.

BASE COUNT 6 a 15 c 12 g 9 t 1 others

ORIGIN

Query Match 0.8%; Score 21.2; DB 9; Length 43;
Best Local Similarity 67.4%; Pred. No. 2.3e+05;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1761 GGGGAAACCTTTATGTGCGAGGTGTGCAACAGTTTC 1803
111 111 111 111 111 111 111 111 111 111
43 GGGAGAAACCTTCNAAGTGCCTGCGCAGAGGCTTCC 1

RESULT 33
LOCUS R75644 49 bp mRNA linear EST 06-JUN-1995
DEFINITION Y159F01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:143545 3' similar to SP:S40468 S40468 PROTEASOME SUBUNIT
RC10-II - ; mRNA sequence.
R75644 R75644.1 GI:850326

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 49)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kuocaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
R., Williamson, A., Wohlmann, P. and Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Insert Size: 848
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert length: 848 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

1. 49
/organism="Homo sapiens"
/db_xref="CDB:552718"
/db_xref="taxon:9606"
/clone="IMAGE:143545"
/clone_lib="Soares placenta Nb2HP"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="PH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGGAAGATTCGGCGCGAGGATTTTATTTTATTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldi.

BASE COUNT 11 a 12 c 10 g 14 t 2 others

ORIGIN

Query Match 0.8%; Score 21.2; DB 14; Length 49;
Best Local Similarity 72.2%; Pred. No. 2.6e+05;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1174 GGCTCAACCTTATGTGCAAGAAATGCGCAGA 1209
111 111 111 111 111 111 111 111 111 111
45 GGCTGAACCTGTATNAGTTCAGAGGCGCAGA 10

RESULT 34
LOCUS AU105724 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU105724 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone.
KAT10272, mRNA sequence.
AU105724 AU105724.1 GI:13555245

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Talra, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

CONTACT: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT10272"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"

BASE COUNT 7 a 6 c 17 g 20 t

ORIGIN

Query Match 0.8%; Score 21.2; DB 9; Length 50;
Best Local Similarity 64.0%; Pred. No. 2.6e+05;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 584 AGATCAGAAACACAGCAGATCATTCCTTTAGTGGCAAGCAGAT 633
111 111 111 111 111 111 111 111 111 111
50 AACACACATCAACAGCGCGACACTGATGATTCACCAAAAT 1

RESULT 35
LOCUS B02962 51 bp DNA linear GSS 13-JUL-1996
DEFINITION CSRL-164B7-u CSRL flow sorted Chromosome 11 specific cosmid Homo
sapiens genomic clone CSRL-164B7, DNA sequence.
ACCESSION B02962 B02962.1 GI:1412240
VERSION
KEYWORDS
SOURCE
human.

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Email: radixon@noble.org
Insert Length: 923 Std Error: 0.00
Plate: 048 row: A column: 11
Seq primer: TCACACAGAGAACACGCTATGAC.
FEATURES
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        1..52
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            /db_xref="taxon:3880"
            /clone="NF048A11ST"
            /clone_lib="Developing stem"
            /tissue_type="stem"
            /dev_stage="Pooled developmental"
            /note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
BASE COUNT
    14 a 16 c 2 g 20 t
ORIGIN
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Best Local Similarity 69.0%; Pred. No. 2.7e+05;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0

Oy 321 CTGCTCTCACGGAATTCATCTCTTCTTAACCAAACTCATT 362
    11 111 1 1 11 1111 11111111 11
Db 6 CTCTCTTCATCACTTGTCAACTTCTCAACCAAAACTCTTT 47

RESULT 37
LOCUS AZ595836 40 bp DNA linear GSS 13-DEC-2000
DEFINITION IM04080008R Mouse 10kb plasmid U0GC1M library Mus musculus genomic
clone U0GC1M0408008 R, DNA sequence.
ACCESSION AZ595836
VERSION AZ595836.1 GI:11718026
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 40)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0408 row: 0 column: 08
Seq primer: CACACAGAGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
    1..40
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="U0GC1M0408008"
        /clone_lib="Mouse 10kb plasmid U0GC1M library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hybridized initially to a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (9114732114191aF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
2 a 8 c 12 g 18 t

Query Match 0.8%; Score 21; DB 17; Length 40;
Best Local Similarity 73.0%; Pred. No. 2.6e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 715 CTGAGAACACAGCCAGCAGTCCAGAGAGACAA 751
DB 37 CTGGAAGACAGACAGCTGCACAGCCCAAGAAACAA 1

RESULT 38
LOCUS AU256802/c 42 bp mRNA linear EST 25-APR-2002
DEFINITION AU256802 3'-directed mouse cDNA library Mus musculus cDNA clone
ACCESSION BE00008995 3', mRNA sequence.
VERSION AU256802
KEYWORDS AU256802.1 GI:20320800
SOURCE EST.
ORGANISM house mouse.
MUS musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS 1 (bases 1 to 42)
TITLE Kato, K. and Matoba, R.
JOURNAL Generation of expressed sequence tags from mouse brain
COMMENT Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatobds.aist-nara.ac.jp,
URL: http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers

FEATURES

source
1..42
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0008995"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy"
BASE COUNT
ORIGIN
16 a 10 c 14 g 2 t

Query Match 0.8%; Score 21; DB 9; Length 42;
Best Local Similarity 82.8%; Pred. No. 2.6e+05;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2472 TGTCTCCATTGGTGTGCTTCTCTCCG 2500
DB 40 TGTCTCTATTGTGGGCTTCCCGC 12

RESULT 39
LOCUS AU103658 50 bp mRNA linear EST 30-AUG-2001

DEFINITION AU103658 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP03969, mRNA sequence.

ACCESSION AU103658
VERSION AU103658.1 GI:13553179
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)

REFERENCE

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

MEDLINE

COMMENT

Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ems.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES

source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP03969"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT
ORIGIN
11 a 7 c 13 g 14 t 5 others

Query Match 0.8%; Score 21; DB 9; Length 50;
Best Local Similarity 73.0%; Pred. No. 3e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 214 TGGCATTCAGGATGTGGCTGTCTACTCACCAGCA 250
DB 14 TGACATTTAGGATGTGGCATGATCTCTCTGCA 50

RESULT 40
LOCUS AU105956/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU105956 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION INEC00029, mRNA sequence.
VERSION AU105956
KEYWORDS AU105956.1 GI:13555477
SOURCE EST.
ORGANISM human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)

REFERENCE

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

MEDLINE

COMMENT

Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ems.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INEC0029"
/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
13 a 8 c 17 g 12 t

ORIGIN

Query Match 0.8%; Score 21; DB 9; Length 50;
Best Local Similarity 73.0%; Pred. No. 3e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 99 CGCGGTGACACCGCGTTCATCTCTCTTGACACTT 135
50 CGCGCGCACGACACTCAATTTCTTTCAGACTT 14

RESULT 41
AA976008/c 58 bp mRNA linear EST 23-JUL-1998
LOCUS c929p04.s1 NCI-CGAP-GC4 Homo sapiens cDNA clone IMAGE:1587727 3.
DEFINITION similar to SW:ZM27_HUMAN P17033 ZINC FINGER PROTEIN 27 ;, mRNA
sequence.
AA976008
AA976008.1 GI:3151800
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 58)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 453 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .58
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1587727"
/clone_1lb="NCI-CGAP-GC4"
/tissue_type="Pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified
polylinker. 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pRTT3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldi."

BASE COUNT
15 a 15 c 15 g 13 t

ORIGIN

Query Match 0.8%; Score 21; DB 9; Length 58;

Best Local Similarity 62.3%; Pred. No. 3.3e+05;
Matches 33; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db 1677 GCGAGAACCCATTGTATGTGCGTGGAGAGAGCTTATATGTAAGTC 1129
58 GGAGGAACGCCCTATACGTGTGATGCGTGGAAAACCTTCATTCGCTC 6

RESULT 42
AV957851 49 bp mRNA linear EST 14-MAR-2002
LOCUS AV957851 Nori Satoh unpublished cDNA library, egg ciona
DEFINITION intestinalis cDNA clone c1eg09a19 5', mRNA sequence.
AV957851
AV957851.1 GI:19446150
EST.
SOURCE Ciona intestinalis.
ORGANISM Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 49)
Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
Expressed genes in Ciona intestinalis
unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .49
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="c1eg09a19"
/clone_1lb="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev-stage="egg"
/note="Vector: pBluescript SK"

BASE COUNT
24 a 7 c 10 g 8 t

ORIGIN

Query Match 0.8%; Score 20.8; DB 10; Length 49;
Best Local Similarity 70.0%; Pred. No. 3.4e+05;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 2348 GGTCAAGTATGATGTGCGAGGAGCAATGATCCCA 2387
2 GCTCAGGTGTGATGATGACAGCAAGTCAAAATCCAA 41

RESULT 43
AZ666147/c 56 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0548C04F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0548C04 F, DNA sequence.
AZ666147
AZ666147.1 GI:11803293
GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 56)
Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss

JOURNAL
COMMENT

[illegible]

LOCUS BH662808 55 bp DNA linear GSS 05-AUG-2002
DEFINITION SALK_090646 Arabidopsis thaliana TDNA insertion lines Arabidopsids
ACCESSION BHE62808
VERSION BHE62808.1 GI:22098134
SOURCE thaliana genomic clone SALK_090646, DNA sequence.
ORGANISM Arabidopsis thaliana
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheek,R., Gadgilnab,
1 (bases 1 to 55) 'Jimmerman,J., Karnes,M., Kim,C.Y., Parker,H., Prednis,L., Shinn,P.
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheek,R., Gadgilnab,
'Zimmerman,J., Karnes,M., Kim,C.Y., Parker,H., Prednis,L., Shinn,P.
A Sequence Indexed Library of Insertion Mutations in the
Arabidopsis Genome Unpublished (2001)
JOURNAL COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckeres@salik.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
Atg9l4120.
Class: TDNA tagged.

FEATURES SOURCE

1..55 /organism="Arabidopsis thaliana" /strain="Columbia 0" /db_xref="taxon:3702" /clone="SALK_090646" /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/dna_protocols.html"	location/Qualifiers
---	---------------------

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Query Match      0.7%; Score 20.6; DB 17; Length 55;
Best Local Similarity   62.7%; Pred.No.4.2e+05;
Matches    32; Conservative     0; Mismatches    19; Indels       0; Gaps      0.

OY          767 AGGCTCCAGCCCTGAACGGAGCGCATCTAGAGGAACAAGCAATATT 817
              || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db           53 AGCATTTCTCCGCCGGGC GGAGAAGAACAAGCAACCAGAAAGCATT 3

RESULT 49
AI955368/c                58 bp mRNA linear EST 19-Aug-1999
LOCUS AI955368             wt12e07.x1 NCI_CGAP UTI Homo sapiens CDNA clone IMAGE:2507258 3'
DEFINITION similar to TR.Q15918 Q15918 ZINC FINGER ; , mRNA sequence.
ACCESSION AI955368
VERSION AI955368.1 GI:5747678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiade; Homo.
REFERENCE 1 (bases 1 to 56) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
COMMENT Unpublished (1997)
CONTACT Robert Strausberg, Ph.D.
EMAIL cgabs@mail.nhl.gov
```

Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLB at:
[www-bio.lnl.gov/bdbp/image/image.html](http://www.bio.lnl.gov/bdbp/image/image.html)

Trace considered overall poor quality
Seq primer: -40UP from Glbco
High quality sequence stop: 1.
Location/Qualifiers

1..58
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2507258"
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adenocarcinoma, 7. pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1; Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Life Technologies catalog #: 1158-014"

BASE COUNT 15 a 11 c 12 g 20 t

ORIGIN

Query Match 0.7%; Score 20.6; DB 9; Length 58;
Best Local Similarity 62.7%; Pred. No. 4.4e+05;
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1347 AAGCCTTACATTTCCAGCGACTGTGAGCAAGCTTTACCAGAACTCACAC 1397
 || ||| ||| || | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 AAACCTAACAAATGTAATGATGTGGCAGAGTCCTTGCGACAAATTCTCAC 8

RESULT 50
LOCUS A2766605 50 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0564L13P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION A2766605
VERSION A2766605.1 GI:12883846
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 50)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rogace,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddunngenet@utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0564 row: L column: 13
 Seq primer: CGTGTAAACGACGCCCATGT
 Class: plasmid ends
 High quality sequence stop: 50.
 Location/Qualifiers

1..50
/organism="Mus musculus"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564L13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-."
/notes="Vector: PWD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      6 a      13 c      20 g      11 t
ORIGIN

```

```

Query Match      0.7%; Score 20.4; DB 17; Length 50;
Best Local Similarity 65.2%; Pred. No. 4.5e+05;
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```

```

QY      2652 TCAGCTGCAGTACGAGAAATTCACCCCTGCTGTGAGGTGGGGA 2697
      |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1 TCAGTGTGTTAGGACACCTGACCCCTGCTGTGAGGTGGGGA 46

```

Search completed: June 4, 2003, 10:24:23
Job time : 3924 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 05:31:36 ; Search time 610 Seconds
(without alignments)
10233.671 Million cell updates/sec

Title: US-09-898-556a-3

Perfect score: 2772

Sequence: 1 cagcgcgctgaagctggtg.....ttctaccatccacacct 2772

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2274872

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

1: N.Geneseq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	2.2	60	24	ABN34034
2	49.4	1.8	51	23	ABL00474
3	49.4	1.8	51	23	ABL00878
4	35	1.3	60	24	ABN33915
5	34.6	1.2	51	22	AA177643
6	33.6	1.2	51	22	AA176919
7	33	1.2	51	22	AA177642
8	31.6	1.1	51	22	AA126920
9	31	1.1	60	24	ABN33655

10	30.6	1.1	60	24	ABN34117	Human spliced tran
11	29.6	1.1	60	24	ABN34244	Human spliced tran
12	28.6	1.0	60	24	ABN34405	Human spliced tran
13	28.6	1.0	60	24	ABN47634	Human spliced tran
14	27.6	1.0	51	22	AA179453	Human silent SNP c
15	27.6	1.0	51	22	AA178093	Human silent SNP c
16	27	1.0	60	24	AA178093	Human silent SNP c
17	26.8	1.0	51	22	AA178093	Human silent SNP c
18	26.8	1.0	51	22	AA178093	Human silent SNP c
19	26.6	1.0	51	22	AA178093	Human silent SNP c
20	26.6	1.0	51	22	AA178093	Human silent SNP c
21	26.6	1.0	51	22	AA178093	Human silent SNP c
22	26.6	1.0	51	22	AA178093	Human silent SNP c
23	26.2	0.9	51	22	AA178093	Human silent SNP c
24	26	0.9	51	22	AA178093	Human silent SNP c
25	25.8	0.9	60	24	ABN33623	Human spliced tran
26	25.6	0.9	60	24	ABN33623	Human spliced tran
27	25.6	0.9	60	24	ABN33623	Human spliced tran
28	25.4	0.9	60	24	ABN33623	Human spliced tran
29	25.2	0.9	60	24	ABN33623	Human spliced tran
30	25.2	0.9	60	24	ABN33623	Human spliced tran
31	25.2	0.9	60	24	ABN33623	Human spliced tran
32	25.2	0.9	60	24	ABN33623	Human spliced tran
33	25	0.9	60	24	ABN33623	Human spliced tran
34	25	0.9	60	24	ABN33623	Human spliced tran
35	24.8	0.9	60	24	ABN33623	Human spliced tran
36	24.8	0.9	60	24	ABN33623	Human spliced tran
37	24.8	0.9	60	24	ABN33623	Human spliced tran
38	24.6	0.9	60	24	ABN33623	Human spliced tran
39	24.6	0.9	60	24	ABN33623	Human spliced tran
40	24.6	0.9	60	24	ABN33623	Human spliced tran
41	24.6	0.9	60	24	ABN33623	Human spliced tran
42	24.6	0.9	60	24	ABN33623	Human spliced tran
43	24.6	0.9	60	24	ABN33623	Human spliced tran
44	24.6	0.9	60	24	ABN33623	Human spliced tran
45	24.4	0.9	60	24	ABN33623	Human spliced tran
46	24.4	0.9	60	24	ABN33623	Human spliced tran
47	24.4	0.9	60	24	ABN33623	Human spliced tran
48	23.8	0.9	60	24	ABN33623	Human spliced tran
49	23.8	0.9	60	24	ABN33623	Human spliced tran
50	23.8	0.9	60	24	ABN33623	Human spliced tran
51	23.8	0.9	60	24	ABN33623	Human spliced tran
52	23.8	0.9	60	24	ABN33623	Human spliced tran
53	23.8	0.9	60	24	ABN33623	Human spliced tran
54	23.6	0.9	60	24	ABN33623	Human spliced tran
55	23.6	0.9	60	24	ABN33623	Human spliced tran
56	23.4	0.8	60	24	ABN33623	Human spliced tran
57	23.2	0.8	60	24	ABN33623	Human spliced tran
58	23	0.8	60	24	ABN33623	Human spliced tran
59	23	0.8	60	24	ABN33623	Human spliced tran
60	23	0.8	60	24	ABN33623	Human spliced tran
61	23	0.8	60	24	ABN33623	Human spliced tran
62	23	0.8	60	24	ABN33623	Human spliced tran
63	23	0.8	60	24	ABN33623	Human spliced tran
64	22.8	0.8	60	24	ABN33623	Human spliced tran
65	22.8	0.8	60	24	ABN33623	Human spliced tran
66	22.6	0.8	60	24	ABN33623	Human spliced tran
67	22.4	0.8	60	24	ABN33623	Human spliced tran
68	22.4	0.8	60	24	ABN33623	Human spliced tran
69	22.4	0.8	60	24	ABN33623	Human spliced tran
70	22.4	0.8	60	24	ABN33623	Human spliced tran
71	22.4	0.8	60	24	ABN33623	Human spliced tran
72	22.2	0.8	60	24	ABN33623	Human spliced tran
73	22.2	0.8	60	24	ABN33623	Human spliced tran
74	22.2	0.8	60	24	ABN33623	Human spliced tran
75	22.2	0.8	60	24	ABN33623	Human spliced tran
76	22.2	0.8	60	24	ABN33623	Human spliced tran
77	22.2	0.8	60	24	ABN33623	Human spliced tran
78	22.2	0.8	60	24	ABN33623	Human spliced tran
79	22.2	0.8	60	24	ABN33623	Human spliced tran
80	22	0.8	60	24	ABN33623	Human spliced tran
81	21.8	0.8	60	24	ABN33623	Human spliced tran
82	21.8	0.8	60	24	ABN33623	Human spliced tran

83	21.8	0.8	60	24	ABN34039	Human spliced tran	C 156	20.2	0.7	51	22	AA130203	Human SNP oligonuc
84	21.8	0.8	60	24	ABN34100	Human spliced tran	157	20.2	0.7	60	19	AAV19098	Synthetic Streptom
C 85	21.8	0.8	60	24	ABA03561	Relaxin/IGF/insull	158	20.2	0.7	60	19	AAV18002	PCR primer used to
C 86	21.6	0.8	41	13	AAO26571	Triplex PCR primer	C 159	20.2	0.7	60	24	AAO37838	Human FHL transme
87	21.6	0.8	41	24	ABA05347	Human zinc finger	C 160	20.2	0.7	60	24	ABN32242	Human spliced tran
88	21.6	0.8	60	24	ABN33990	Human spliced tran	C 161	20.2	0.7	60	24	ABN33459	Human spliced tran
C 89	21.4	0.8	31	22	AA130914	Human single nucle	C 162	20.2	0.7	60	24	ABN34836	Human spliced tran
C 90	21.4	0.8	50	22	AA132254	Human SNP oligonuc	C 163	20.2	0.7	60	24	ABN42196	Human spliced tran
C 91	21.4	0.8	51	22	AA176047	Human silent SNP c	C 164	20.2	0.7	60	24	ABN46051	Human spliced tran
C 92	21.4	0.8	60	24	ABN36823	Human spliced tran	C 165	20.2	0.7	60	24	ABN47576	Human spliced tran
C 93	21.4	0.8	60	24	ABN48558	Human spliced tran	C 166	20.2	0.7	60	24	ABN48331	Human spliced tran
C 94	21.4	0.8	60	24	AAO29929	Human spliced tran	C 167	20.2	0.7	60	24	ABN48650	Human spliced tran
C 95	21.2	0.8	50	22	AA127943	Human SNP oligonuc	C 168	20.2	0.7	41	24	ABL40933	Human zinc finger
C 96	21.2	0.8	50	22	AA175119	Human silent SNP c	C 169	20.2	0.7	42	20	AAO12365	Human chromosome 1
C 97	21.2	0.8	50	22	AA175119	Human probe #8. H	C 170	20.2	0.7	44	12	AAO12365	Probe 13 based on
C 98	21.2	0.8	60	24	ABN33526	Human spliced tran	C 171	20.2	0.7	44	13	AAO35070	Probe 13 for detec
C 99	21.2	0.8	60	24	ABN33725	Human spliced tran	C 172	20.2	0.7	47	21	AAO26941	Human map-related
100	21.2	0.8	60	24	ABN34378	Human spliced tran	C 173	20.2	0.7	48	16	AAO81434	HBV target sequenc
101	21.2	0.8	40	21	AAO88433	Thiamine responsiv	C 174	20.2	0.7	50	19	AAV30378	Oligomer p50rg16 u
C 102	21.2	0.8	45	24	AAO3634	Three finger DNA a	C 175	20.2	0.7	50	24	AAO35532	Methylomas 16a s
C 103	21.2	0.8	49	17	AA135402	Primer MS-P2 to ce	C 176	20.2	0.7	51	21	AAO77399	Human clone CG4492
C 104	21.2	0.8	50	22	AA135402	S. capricanis smel	C 177	20.2	0.7	51	22	AA127337	Human SNP oligonuc
C 105	21.2	0.8	50	22	AA132253	Human SNP oligonuc	C 178	20.2	0.7	52	22	AAH91974	Human inflammatory
106	21.2	0.8	59	18	AA157984	Truncated P-select	C 179	20.2	0.7	54	20	AAO21943	Fragment of the VD
107	21.2	0.8	60	24	ABN40788	Human spliced tran	C 180	20.2	0.7	55	21	AAO65685	Human BPI PCR prim
C 108	21.2	0.8	60	24	ABN48819	Human spliced tran	C 181	20.2	0.7	60	24	ABN33155	Human spliced tran
C 109	21.2	0.8	60	24	ABN50298	Human spliced tran	C 182	20.2	0.7	60	24	ABN33264	Human spliced tran
C 110	20.8	0.8	33	22	AAH43217	Human zinc-finger	C 183	20.2	0.7	60	24	ABN33445	Human spliced tran
C 111	20.8	0.8	41	22	AAH76682	Human zinc-finger	C 184	20.2	0.7	60	24	ABN33716	Human spliced tran
C 112	20.8	0.8	41	22	AAO42068	Novel murine zinc	C 185	20.2	0.7	60	24	ABN33813	Human spliced tran
C 113	20.8	0.8	41	16	AAO87598	Primer for PCR ampl	C 186	20.2	0.7	60	24	ABN34721	Human spliced tran
C 114	20.8	0.8	48	16	AAO85335	PCR primer for fragmen	C 187	20.2	0.7	60	24	ABN37226	Human spliced tran
C 115	20.8	0.8	51	22	AA127314	Human SNP oligonuc	C 188	20.2	0.7	60	24	ABN37979	Human spliced tran
C 116	20.8	0.8	51	23	AB100548	Human silent nonco	C 189	20.2	0.7	60	24	ABN39834	Human spliced tran
C 117	20.8	0.8	60	24	ABN33735	Human spliced tran	C 190	20.2	0.7	60	24	ABN42034	Human spliced tran
C 118	20.8	0.8	60	24	ABN33917	Human spliced tran	C 191	20.2	0.7	60	24	ABN43740	Human spliced tran
C 119	20.8	0.8	60	24	ABN43176	Human spliced tran	C 192	20.2	0.7	60	24	ABN46638	Human spliced tran
C 120	20.8	0.8	60	24	ABN44593	Human spliced tran	C 193	20.2	0.7	60	24	ABN48545	Human spliced tran
C 121	20.8	0.8	60	24	ABN48210	Human spliced tran	C 194	19.8	0.7	28	21	AAA38456	Murine Sm22 gene C
C 122	20.6	0.7	47	24	ABN17143	Streptococcus agal	C 195	19.8	0.7	41	24	AAZ93777	Human zinc-finger
C 123	20.6	0.7	51	22	AA128100	Human SNP oligonuc	C 196	19.8	0.7	41	24	ABK48079	Human zinc-finger
C 124	20.6	0.7	51	22	AA129371	Human silent SNP c	C 197	19.8	0.7	41	24	ABK48080	Human zinc-finger
C 125	20.6	0.7	51	22	AA178540	Human silent SNP c	C 198	19.8	0.7	47	19	AAV28740	Oligonucleotide SM
C 126	20.6	0.7	51	22	AA178541	Human silent SNP c	C 199	19.8	0.7	47	22	AAO21116	Oligo SME-1, used
C 127	20.6	0.7	52	18	AA157992	Truncated P-select	C 200	19.8	0.7	47	22	AAO20575	Mouse SME-2, alpha 1
C 128	20.6	0.7	60	24	ABN33972	Human spliced tran	C 201	19.8	0.7	47	22	AAO26689	Human obesity-asso
C 129	20.6	0.7	60	24	ABN33532	Human spliced tran	C 202	19.8	0.7	47	24	ABK40917	Electrophoretic mo
C 130	20.6	0.7	60	24	ABN35918	Human spliced tran	C 203	19.8	0.7	47	24	ABK33341	Human SNP oligonuc
C 131	20.6	0.7	60	24	ABN38523	Human spliced tran	C 204	19.8	0.7	50	22	AA130970	Human SNP oligonuc
C 132	20.6	0.7	60	24	ABN50535	Human spliced tran	C 205	19.8	0.7	50	22	AA176271	Human silent SNP c
C 133	20.4	0.7	41	24	ABA98015	Human superoxide d	C 206	19.8	0.7	51	22	AA127049	Human SNP oligonuc
C 134	20.4	0.7	41	24	ABA04288	Human sex determin	C 207	19.8	0.7	51	22	AA174524	Human silent SNP c
C 135	20.4	0.7	45	21	AAZ96671	T cell antigen rec	C 208	19.8	0.7	51	22	AA174524	Human silent SNP c
C 136	20.4	0.7	50	22	AA129955	Human SNP oligonuc	C 209	19.8	0.7	51	22	AA176039	Human silent SNP c
C 137	20.4	0.7	51	22	AA127636	Human SNP oligonuc	C 210	19.8	0.7	51	22	AA176566	Human amino acid c
C 138	20.4	0.7	51	22	AA174659	Human silent SNP c	C 211	19.8	0.7	57	20	AAO10876	PCR primer used to
C 139	20.4	0.7	54	20	AAV84652	PCR primer used to	C 212	19.8	0.7	58	21	AAO13951	Human secreted pro
C 140	20.4	0.7	60	24	ABN32547	Human spliced tran	C 213	19.8	0.7	59	20	AAZ22491	Oligonucleotide se
C 141	20.4	0.7	60	24	ABN38013	Human spliced tran	C 214	19.8	0.7	60	16	AAO98853	Anti-human IL-4 hu
C 142	20.4	0.7	60	24	ABN39542	Human spliced tran	C 215	19.8	0.7	60	16	AAV75972	Staphylococcus aur
C 143	20.4	0.7	60	24	ABN40506	Human spliced tran	C 216	19.8	0.7	60	16	AAV75972	Human spliced tran
C 144	20.4	0.7	60	24	ABN42336	Human spliced tran	C 217	19.8	0.7	60	24	ABN32367	Human spliced tran
C 145	20.4	0.7	60	24	ABN43789	Human spliced tran	C 218	19.8	0.7	60	24	ABN33529	Human spliced tran
C 146	20.4	0.7	60	24	ABN44217	Human spliced tran	C 219	19.8	0.7	60	24	ABN34919	Human spliced tran
C 147	20.4	0.7	60	24	ABN44689	Human spliced tran	C 220	19.8	0.7	60	24	ABN35263	Human spliced tran
C 148	20.4	0.7	60	24	ABN48107	Human spliced tran	C 221	19.8	0.7	60	24	ABN43641	Human spliced tran
C 149	20.4	0.7	60	24	ABN50256	Human spliced tran	C 222	19.8	0.7	60	24	ABN44277	Human spliced tran
C 150	20.2	0.7	41	24	ABA03772	Human zinc finger	C 223	19.8	0.7	60	24	ABN45332	Human spliced tran
C 151	20.2	0.7	41	24	ABA05348	Human zinc finger	C 224	19.8	0.7	60	24	ABN46381	Human spliced tran
C 152	20.2	0.7	47	21	AAO26584	Human map-related	C 225	19.8	0.7	60	24	ABN47162	Human spliced tran
C 153	20.2	0.7	50	15	AAO70985	PCNA gene specific	C 226	19.8	0.7	60	24	ABN49599	Human spliced tran
C 154	20.2	0.7	50	22	AA128938	Human SNP oligonuc	C 227	19.8	0.7	60	24	ABN49864	Human spliced tran
C 155	20.2	0.7	51	22	AA128074	Human SNP oligonuc	C 228	19.8	0.7	60	24	ABN50011	Human spliced tran

C 375	19	0.7	45	24	ABAO1543	MyCamtrose biosyrit
C 376	19	0.7	46	22	AAD19782	Human ST drug-meta
C 377	19	0.7	48	24	AAD33621	OTS-008 primer use
C 378	19	0.7	48	24	ABK22526	Human ERG ambrzym
C 379	19	0.7	50	20	AAO06711	:HBV, LLA2C.75 amp1
C 380	19	0.7	50	20	AAK53307	Probe used to Isol
C 381	19	0.7	50	21	AAAS4096	Probe for PRO228 c
C 382	19	0.7	50	21	AAZ93491	Prob for PRO228 cD
C 383	19	0.7	50	22	AAAL33956	Human SNP oligonuc
C 384	19	0.7	50	22	AAAL34154	Human SNP oligonuc
C 385	19	0.7	50	22	AAAF72465	Human PRO polypept
C 386	19	0.7	50	22	AAAC97436	Human PRO228 hyd:1
C 387	19	0.7	51	22	AAAL27615	Human SNP oligonuc
C 388	19	0.7	51	22	AAAL28103	Human SNP oligonuc
C 389	19	0.7	51	22	AAAL28592	Human SNP oligonuc
C 390	19	0.7	51	22	AAAL29235	Human SNP oligonuc
C 391	19	0.7	51	22	AAAL32937	Human SNP oligonuc
C 392	19	0.7	51	22	AAAL33010	Human SNP oligonuc
C 393	19	0.7	51	22	AAAL74758	Human silent SNP c
C 394	19	0.7	51	22	AAAL76764	Human silent SNP c
C 395	19	0.7	51	22	AAAL78672	Human silent SNP c
C 396	19	0.7	51	22	AAAL79706	Human conservative
C 397	19	0.7	51	22	AAAH96607	Human DNA containi
C 398	19	0.7	51	22	AAAH96616	Human SNP flanki:ng
C 399	19	0.7	51	23	ABLU00455	Human silent nonco
C 400	19	0.7	54	17	AAAT34305	Primer NOTKINCYS f
C 401	19	0.7	55	21	AAAC29085	Human secreted pro
C 402	19	0.7	57	17	AAAT28358	HCY primer used in
C 403	19	0.7	59	21	AAAT296824	S. cerevisiae gene
C 404	19	0.7	60	22	AAAF31238	Novel BMC vector c
C 405	19	0.7	60	24	ABN33712	Human spliced tran
C 406	19	0.7	60	24	ABN33743	Human spliced tran
C 407	19	0.7	60	24	ABN34130	Human spliced tran
C 408	19	0.7	60	24	ABN34393	Human spliced tran
C 409	19	0.7	60	24	ABN35543	Human spliced tran
C 410	19	0.7	60	24	ABN36348	Human spliced tran
C 411	19	0.7	60	24	ABN36684	Human spliced tran
C 412	19	0.7	60	24	ABN36837	Human spliced tran
C 413	19	0.7	60	24	ABN38197	Human spliced tran
C 414	19	0.7	60	24	ABN39382	Human spliced tran
C 415	19	0.7	60	24	ABN40173	Human spliced tran
C 416	19	0.7	60	24	ABN40183	Human spliced tran
C 417	19	0.7	60	24	ABN42743	Human spliced tran
C 418	19	0.7	60	24	ABN42984	Human spliced tran
C 419	19	0.7	60	24	ABN43567	Human spliced tran
C 420	19	0.7	60	24	ABN44449	Human spliced tran
C 421	19	0.7	60	24	ABN44493	Human spliced tran
C 422	19	0.7	60	24	ABN45251	Human spliced tran
C 423	19	0.7	60	24	ABN46757	Human spliced tran
C 424	19	0.7	60	24	ABN46802	Human spliced tran
C 425	19	0.7	60	24	ABN46969	Human spliced tran
C 426	19	0.7	60	24	ABN47943	Human spliced tran
C 427	19	0.7	60	24	ABN49054	Human spliced tran
C 428	19	0.7	60	24	ABN49123	Human spliced tran
C 429	19	0.7	60	24	ABN50617	Human spliced tran
C 430	19	0.7	60	24	ABN58522	Human spliced tran
C 431	19	0.7	60	24	AAAD29928	Oligonucleotide us
C 432	18.8	0.7	31	22	AAI30916	Human single nucle
C 433	18.8	0.7	40	22	AAAF75943	TMV-based random 1
C 434	18.8	0.7	40	22	AAAF60055	Oligonucleotide #1
C 435	18.8	0.7	41	24	ABLA0716	Human myosin heavy
C 436	18.8	0.7	41	24	ABLA0717	Human myosin heavy
C 437	18.8	0.7	41	24	ABAA98014	Human superoxide d
C 438	18.8	0.7	41	24	ABAA95342	Human endoprotease
C 439	18.8	0.7	47	21	AAZ65903	Human map-related
C 440	18.8	0.7	47	21	AAZ66003	Human map-related
C 441	18.8	0.7	47	21	AAZ66884	Human map-related
C 442	18.8	0.7	47	21	AAZ68911	Human map-related
C 443	18.8	0.7	49	13	AAO35798	H6 promoter/HN gen
C 444	18.8	0.7	49	20	AAAV5035	Human E124 PCR 3r1
C 445	18.8	0.7	50	22	AAAL27942	Human SNP oligonuc
C 446	18.8	0.7	50	22	AAAL30708	Human SNP oligonuc
C 447	18.8	0.7	50	22	AAAT78135	Human silent SNP c

448	18.8	0.7	50	22	AAD03092	1467-04 oligonucle
449	18.8	0.7	50	24	ABL59727	Mycobacterium tube
C 450	18.8	0.7	51	22	AAAL29922	Human SNP oligonuc
C 451	18.8	0.7	51	22	AAD17720	V. parahaemolyticu
C 452	18.8	0.7	51	22	AAI74658	Human silent SNP c
C 453	18.8	0.7	51	22	AAI75286	Human silent SNP c
C 454	18.8	0.7	51	22	AAI76527	Human silent SNP c
C 455	18.8	0.7	51	22	AAI76883	Human silent SNP c
C 456	18.8	0.7	51	22	AAH89547	Human coding sequ
C 457	18.8	0.7	51	22	AAH79930	Human DNA containi
C 458	18.8	0.7	53	19	AAV04151	PCR product used i
C 459	18.8	0.7	54	22	AAAS04528	Gene expression pr
C 460	18.8	0.7	56	22	AAAF29832	Library component
C 461	18.8	0.7	57	21	AAAO5800	p12 library varian
C 462	18.8	0.7	58	21	AAAC11140	Human secreted pro
C 463	18.8	0.7	59	22	AAD06903	Human Oligo 11 to
C 464	18.8	0.7	59	24	ABQ73670	Murine FST1 anlis
C 465	18.8	0.7	60	21	AAAC5888	Eucalyptus grandis
C 466	18.8	0.7	60	24	ABN32924	Human spliced tran
C 467	18.8	0.7	60	24	ABN33211	Human spliced tran
C 468	18.8	0.7	60	24	ABN33872	Human spliced tran
C 469	18.8	0.7	60	24	ABN34550	Human spliced tran
C 470	18.8	0.7	60	24	ABN35020	Human spliced tran
C 471	18.8	0.7	60	24	ABN35624	Human spliced tran
C 472	18.8	0.7	60	24	ABN35870	Human spliced tran
C 473	18.8	0.7	60	24	ABN36616	Human spliced tran
C 474	18.8	0.7	60	24	ABN36882	Human spliced tran
C 475	18.8	0.7	60	24	ABN37407	Human spliced tran
C 476	18.8	0.7	60	24	ABN37451	Human spliced tran
C 477	18.8	0.7	60	24	ABN38146	Human spliced tran
C 478	18.8	0.7	60	24	ABN38623	Human spliced tran
C 479	18.8	0.7	60	24	ABN38895	Human spliced tran
C 480	18.8	0.7	60	24	ABN38931	Human spliced tran
C 481	18.8	0.7	60	24	ABN40848	Human spliced tran
C 482	18.8	0.7	60	24	ABN41311	Human spliced tran
C 483	18.8	0.7	60	24	ABN41595	Human spliced tran
C 484	18.8	0.7	60	24	ABN42970	Human spliced tran
C 485	18.8	0.7	60	24	ABN44311	Human spliced tran
C 486	18.8	0.7	60	24	ABN44616	Human spliced tran
C 487	18.8	0.7	60	24	ABN45168	Human spliced tran
C 488	18.8	0.7	60	24	ABN48830	Human spliced tran
C 489	18.6	0.7	25	21	AAAI2188	Human MTF DNA pri
C 490	18.6	0.7	25	24	ABN14634	Human GMLP-1 25-m
C 491	18.6	0.7	27	21	AAZ51744	N-terminal primer
C 492	18.6	0.7	36	16	AAZ55895	Human TNF-alpha ha
C 493	18.6	0.7	38	21	AAZ47336	PCR primer sexole
C 494	18.6	0.7	39	19	AAAV29416	Calcium ion channe
C 495	18.6	0.7	42	18	AAV04442	Antisense primer f
C 496	18.6	0.7	43	21	AAZ45516	Primer Barnaseh102
C 497	18.6	0.7	45	12	AAO12264	Probe to mislaset
C 498	18.6	0.7	45	24	ABAO4690	Peptide B2.7 codin
C 499	18.6	0.7	46	20	AAAI9349	Oligonucleotide LA
C 500	18.6	0.7	47	15	AAO68630	A33 heavy chain va

ALIGNMENTS

RESULT 1
ID ABR34034 standard; DNA; 60 BP.

AC ABR34034;

DE 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:6782.

XX Human: mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome: oligonucleotide library; ss.

OS Homo sapiens.

XX

PN WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB01903.
XX
XX 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Falgler S;
PI
PI WPI: 2002-257383/30.
XX
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX
XX Example 1; SEQ ID 6782; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 60 BP; 16 A; 15 C; 18 G; 11 T; 0 other:
SO
Query Match 2.2%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1792 GCAGAGCTTTGGCGAGAGCTTAACCTGTTAGGACACAGAGGCGACACTCAGTGCGCT 1851
Db 1 GCAGAGGTTTCGCGAGAGGCTTAACCTGTTAGGACACAGAGGCGACACTCAGTGCGCT 60
RESULT 2
ABL00474/c
ID ABL00474 standard; DNA; 51 BP.
XX
XX ABL00474;
XX
XX 05-MAR-2002 (first entry)
XX
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:465.
DE
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; ds.
XX

OS Homo sapiens.
XX
XX WO200138586-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 22-NOV-2000; 2000WO-US32311.
PE
XX
XX 24-NOV-1999; 99US-0167383.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimkets RA, Leach M;
PI
XX
XX WPI: 2001-355949/37.
DR
XX
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT sequence polymorphism
XX
XX
XX Claim 1; Page 388; 674pp; English.
PS
XX
XX ABL0010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the
CC polymorphic protein within appropriate physiological samples).
XX
XX Sequence 51 BP; 9 A; 10 C; 14 G; 18 T; 0 other:
SO
Query Match 1.8%; Score 49.4; DB 23; Length 51;
Best Local Similarity 98.0%; Pred. No. 2.8e-05;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1378 GCTTTAGCCAGAGTCACACCTCATTCAGACACTTAAGCACACAGAGAG 1428
Db 51 GCTTTAGCCAGAGTCACACCTCATTCAGACACTTAAGCACACAGAGAG 1
RESULT 3
ABL00878/c
ID ABL00878 standard; DNA; 51 BP.
XX
XX ABL00878;
XX
XX 05-MAR-2002 (first entry)
XX
XX Human amino acid change SNP oligonucleotide SEQ ID NO:869.
DE
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200138586-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 22-NOV-2000; 2000WO-US32311.
PE

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XX 24-NOV-1999; 990US-0167383.
PR (CURA-) CURAGEN CORP.
PA
XX Shinkets RA, Leach M;
PI
XX WPI: 2001-355949/37.
DR
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT sequence polymorphism.
XX
PS Claim 1; Page 509; 674pp; English.
PS
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the
CC polymorphic protein within appropriate physiological samples).
XX
SQ Sequence 51 BP; 10 A; 14 C; 12 G; 15 T; 0 other;
Query Match 1.8%; Score 49.4; DB 23; Length 51;
Best Local Similarity 98.0%; Pred. No. 2.8e-05;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1362 AGGAGGTGTGAGCAAGGCTTTAGCCAGAGTACACACCTCATCAGACACTTA 1412
ID 51 AGGAGGTGTGAGCAAGGCTTTAGCCGAGTACACACCTCATCAGACACTTA 1
Db
RESULT 4
ABN33915
ID ABN33915 standard; DNA; 60 BP.
XX
AC ABN33915;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6663.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
WO200210449-A2.
XX
PN 07-FEB-2002.
XX
PD
XX 20-JUL-2001; 2001WO-1B01903.
XX
PE 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI: 2002-257383/30.
DR
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XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes.
XX
PS Example 1; SEQ ID 6663; 47pp; English.
PS
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABB59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 20 A; 19 C; 12 G; 9 T; 0 other;
Query Match 1.3%; Score 35; DB 24; Length 60;
Best Local Similarity 74.6%; Pred. No. 1.1;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1041 GGCTTTCGTCGAGTCAACCTGATCAGACATGAGGAGGACACACAGGAGCAAAAC 1093
ID 1 GCCTTTCCAGAGTCAACCTGATCAGATGATGAGAGAAATGACACAGAGGAGAAAC 59
Db
RESULT 5
AAI77643
ID AAI77643 standard; DNA; 51 BP.
XX
AC AAI77643;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4584.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
WO200140521-A2.
XX
PN 07-JUN-2001.
XX
PD
XX 30-NOV-2000; 2000WO-US32758.
XX
PE 30-NOV-1999; 990US-0168138.
XX
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
```

DR WPI: 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 1913; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 51 BP; 17 A; 14 C; 13 G; 7 T; 0 other;
XX
Query Match 1.2%; Score 34.6; DB 22; Length 51;
Best Local Similarity 81.6%; Pred. No. 1.4;
Matches 40; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
DY 2375 AGTCAATGCCAGCATAGGGGTGGTACCTGTTGAAACCCCACT 2423
ID 1 AGACAATGCTTAGGACATAGGGGTAGGTCACACGTGAACCCCACT 49
AA126919 standard; DNA: 51 BP.
XX
AC AA126919;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #127.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 1434; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP; 19 A; 11 C; 10 G; 11 T; 0 other;
XX
Query Match 1.2%; Score 33.6; DB 22; Length 51;
Best Local Similarity 81.2%; Pred. No. 2.8;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
DY 1057 CAACCTGATTCACATCAGACAGACATCTCAGGGGAGAAACCTTATG 1104
ID 1 CAACCTGATTTGTATCATCAGAGAACATCATACAGAGAGAAACCTATG 48
AA177642 standard; DNA: 51 BP.
XX
AC AA177642;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4583.
XX
KW Human: single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
XX
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI: 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 1913; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AAM5311 to AAM53129 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (1) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally (1) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (1) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.

Query Match	1.2%	Score 33;	DB 22;	Length 51;
Best Local Similarity	79.6%	Pred. No. 4.4;		
Matches 39;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;

DY 2375 AGTCAATGCCAGGCAGATAGGGGTGGTACCTGCTGA AACCCAACT 2423

DB 1 AGACAATGCTTAGGCAGATAGGGGCAGTCACAGATGA AACCCCACT 49

```

RESULT 8
AAL26920
ID      AAL26920 standard; DNA; 51 BP.

```

AA	
AC	AAL26920;
XX	
DT	24-JAN-2002 (first entry)
XX	
DE	Human SNP oligonucleotide #128.
XX	
KM	Immunosuppressive; antinostimulatory; antiinflammatory; cytostatic;
KM	neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KM	amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor
KM	complement related protein; cytochrome; kinesin; cytokine; interferon;
KM	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM	multifactorial disease; autoimmune disease; infection;
KM	nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases
PT oncogenes and histones, useful for diagnosing and treating, e.g.
cancer, autoimmune diseases

PS Claim 1; Page 1434; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

Query Match	1.1%	Score 31.6	DB 22	Length 51
Best Local Similarity	80.4%	Pred. No. 12		
Matches 37, Conservative	0	Mismatches 9	Indels 0	Gaps 0

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QY      1412 AAGCACACACACAGGAGAGAGCCCTTATGTATGCACAGATGTGGG 145
          | | | | | | | | | | | | | | | | | | | | | | | |
Db      2   ACGGATACACACGAGAGAGAGCCCTTATCAGTGCAAGAGATGTGGG 47

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RESULT 9
ABN33655
ID ABN33655 standard; DNA; 60 BP

AA	ADBN33655;		
AC			
DT	15-JUL-2002	(first entry)	
DE	Human spliced transcript detection oligonucleotide	SEQ ID NO:6403	
XX			
XX			
DE	Human; mouse; rat; splice transcript; detection; RNA transcript;		
XX	splice variant; transcripome; oligonucleotide library; ss.		
KN			

05 Homo sapiens

PN WO200210449-A2

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB01903

PR 28-JUL-2000; 2000US-221607P
PR 02-MAY-2001; 2001US-287724P
PR

PA (COMP-) COMPUGEN INC

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30

PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -

PS Example 1; SEQ ID 6403; 47pp; English

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 19 A; 11 C; 20 G; 10 T; 0 other;

Query Match 1.1%; Score 31; DB 24; Length 60;
Best Local Similarity 87.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1419 CACACAGAGAGAGCCTTATGTATGCACAGATGTGG 1457
DB 15 CACACAGAGAGAGCCTTATGTATGCACAGATGTGG 53
|||||

RESULT 10
ABN34117
ID ABN34117 standard; DNA; 60 BP.
XX
AC ABN34117;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6865.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 6865; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 16 A; 12 C; 16 G; 16 T; 0 other;

Query Match 1.1%; Score 30.6; DB 24; Length 60;
Best Local Similarity 73.6%; Pred. No. 28;
Matches 39; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1849 CCTTGTGTGAGGAGTGTGGCAAGCCTTTGTCGTAAGTAACTCATTT 1901
DB 6 CCTTGTGTGCAAGAGTGTGGCAAGCCTTTGTCGTAAGTAACTCATTT 58
|||||

RESULT 11
ABN34244
ID ABN34244 standard; DNA; 60 BP.
XX
AC ABN34244;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6992.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 6992; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX

SO Sequence 60 BP; 21 A; 11 C; 16 G; 12 T; 0 other;

Query Match 1.1%; Score 29.6; DB 24; Length 60;
Best Local Similarity 68.3%; Pred. No. 56;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1576 ACCAGAGGTACACAGCGGAGAGCCATTGTATGTACGAGGAGTGCGGAGGCTTTA 1635
ID 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ATCAGAGAGTCCACACTGTAGAGAAACATTCAATGTGTGATGCGGAGAAAGCTTCA 60

RESULT 12
ABN34405
ID ABN34405 standard; DNA: 60 BP.
XX
XX ABN34405;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:7153.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI: 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes

XX Example 1; SEQ ID 7153; 47pp; English.

PS The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX

SO Sequence 60 BP; 22 A; 17 C; 8 G; 13 T; 0 other;

Query Match 1.0%; Score 28.6; DB 24; Length 60;
Best Local Similarity 67.8%; Pred. No. 1.2e+02;
Matches 40; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1381 TTAGCAGAGTCCACCTCTCATGACACTTAAGACACACAGAGAGAGCTTAT 1439
ID 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 TTAGTCAGAAAGCAGCGCCTCTTTCACCATATCAGATCCACAGACAAAGCTTAT 59

RESULT 13
ABN47634
ID ABN47634 standard; DNA: 60 BP.
XX
XX ABN47634;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:20382.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI: 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes

XX Example 1; SEQ ID 20382; 47pp; English.

PS The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
CC XX

SO Sequence 60 BP; 18 A; 15 C; 15 G; 12 T; 0 other;

Query Match 1.0%; Score 28.6; DB 24; Length 60;
Best Local Similarity 67.8%; Pred. No. 1.2e+02;
Matches 40; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1302 CAGGATTCACACCGTCGACAGACACATTCAGAGAGAGCCCTTCATTG 1360
DB 1 CAGAGCTTCTAACGTGGTGTCTATCACAAGACATGCCAGAGAGACCCCTACCACTG 59

RESULT 14
AA179453
ID AA179453 standard; DNA: 51 BP.
AC AA179453;
XX
DT 09-NOV-2001 (first entry)
XX

DE Human silent SNP containing nucleic acid SEQ:6394.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN W0200140521-A2.
XX
PD 07-JUN-2001.
XX
PE 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
PI Shimkets RA, Leach M;
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 2464; 2653bp; English.
XX

AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA153114 to AA153329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its

CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
CC XX

SO Sequence 51 BP; 16 A; 6 C; 18 G; 11 T; 0 other;

Query Match 1.0%; Score 27.8; DB 22; Length 51;
Best Local Similarity 74.5%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1243 AGAGGGCGCACACTGGGAGAGAGCCTTATGTTCCAGGAAATGCGG 1289
DB 1 AGAGACTCCACACTGAGAGAAACCTTATGATGTGTGATGTGCG 47

RESULT 15
AA178093/C
ID AA178093 standard; DNA: 51 BP.
AC AA178093;
XX
DT 09-NOV-2001 (first entry)
XX

DE Human silent SNP containing nucleic acid SEQ:5034.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN W0200140521-A2.
XX
PD 07-JUN-2001.
XX
PE 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
PI Shimkets RA, Leach M;
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 2050; 2653bp; English.
XX

AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA153114 to AA153329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.

CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.

CC Sequence 51 BP; 13 A; 10 C; 13 G; 15 T; 0 other;

SO Query Match 1.0%; Score 27.6; DB 22; Length 51;

Best Local Similarity 72.0%; Pred. No. 2.2e+02;

Matches 36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1687 CATTTGTAATGTCGAGTGTGACAGGCTTTAATGATAGACGACCCCTC 1736

DB 51 CTTATGATGATGATACAGAGTGTGGGAAGCCTTCAACATGATTCACCCCTC 2

RESULT 16

AAD33614

AD33614 standard; DNA: 60 BP.

AC AAD33614;

DT 01-JUL-2002 (first entry)

DE zif-1 specific PCR primer 1 used to generate three finger ZFP.

XX DNA binding protein; zinc finger domain 1; zinc finger protein; ZFP;

XX viral replication; gene expression; virucide; zif1; PCR; primer; ss.

XX Unidentified.

XX WO200208286-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-EP08367.

XX 21-JUL-2000; 2000US-220060P.

XX WPI: 2002-172000/22.

XX New Zinc Finger Protein (ZFP) comprising three essential domains useful

PT for diagnosing diseases associated with abnormal genomic structure -

XX Example 6; Page 70; 143pp; English.

CC The present invention relates to novel DNA binding proteins comprising

CC zinc finger domains in which two histidine and two cysteine residues

CC coordinate a central zinc ion. The invention particularly relates to

CC the identification of a context-independent recognition code to design

CC zinc finger domains. The invention also relates to zinc finger proteins

CC (ZFP) designed using this recognition code. The ZFPs are useful for

CC altering genomic structure, inhibiting viral replication (where viral

CC replication is inhibited for plant virus, an animal virus or a human

CC virus), modulating gene expression, detecting an altered zinc finger

CC recognition sequence and diagnosing disease associated with abnormal

CC genomic structure. The present DNA sequence is zinc finger domain 1

CC (zif-1) specific PCR primer 1 used to generate three finger ZFP. This

XX sequence is used in the exemplification of the invention.

XX Sequence 60 BP; 15 A; 6 C; 17 G; 13 T; 9 other;

SO Query Match 1.0%; Score 27; DB 24; Length 60;

Best Local Similarity 60.0%; Pred. No. 3.8e+02;

Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1593 GGGGAGAGCCATTGTATGATGAGAGTGTGGCGAGGCTTTACCCGGAATCAACCCCTG .652

DB 1 GGGGAGAGCCGATTAATGTCGGAATGTGTAAAGTTTACGACNNNNNNNNNTTTC 60

RESULT 17

AAL32346

AL32346 standard; DNA: 51 BP.

AC AAL32346;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #5554.

XX Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;

XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;

XX amyloid protein; angiotensin; apoptosis related protein; cadherin;

XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

XX complement related protein; cytochrome; kinesin; cytokine; interferon;

XX interleukin; G-protein coupled receptor; thioesterase; inflammation;

XX multifactorial disease; autoimmune disease; infection;

XX nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

XX oncogenes and histones, useful for diagnosing and treating, e.g.

XX cancer, autoimmune diseases and infections -

XX Claim 1; Page 2986; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic

CC variants of proteins related to amylases, amyloid proteins, angiotensin,

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

CC histones, kinases, colony stimulating factors, complement related

CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,

CC G-protein coupled receptors and thioesterases. The present sequence is

CC one such oligonucleotide. The oligonucleotides and the peptides encoded

CC by them may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the proteins listed

CC above. Disorders that may be prevented, diagnosed and/or treated include

CC multifactorial diseases with a genetic component, such as autoimmune

CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythematosus and Grave's disease), inflammation, cancer

CC (e.g. cancers of the bladder, brain, breast, colon and kidney,

CC leukaemia), diseases of the nervous system and an infection of pathogenic

CC organisms.

XX Sequence 51 BP; 12 A; 9 C; 15 G; 15 T; 0 other;

SO Query Match 1.0%; Score 26.8; DB 22; Length 51;

Best Local Similarity 73.9%; Pred. No. 4e+02;

Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 214 TGGCATTACAGGATGCTGTGTACTTCAACCGAGAGAGTGAG 259

DB 1 TGACTTTTGAAGACGTGCTGTGAATTTTCCACGAGAGATGAG 46

RESULT 18

AAL33199

AL33199 standard; DNA: 51 BP.

XX AAL33199;
 AC
 XX 24-JAN-2002 (first entry)
 DT
 XX
 XX
 DE Human SNP oligonucleotide #6407.
 XX
 KW Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 KW
 OS Homo sapiens.
 OS
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI: 2001-465210/50.
 XX
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections
 XX
 XX Claim 1; Page 3217; 4143pp; English.
 PS
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 CC
 XX
 SQ Sequence 51 BP; 19 A; 17 C; 11 G; 4 T; 0 other;
 XX
 Query Match 1.0%; Score 26.8; DB 22; Length 51;
 Best Local Similarity 73.9%; Pred. No. 4e+02;
 Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0
 QY 1560 TCAAACTTACAAACACGACAGGTCACACAGCGGGAGAGCCAT 1605
 1111111 111 11111 1 11111 11 1111 111 1
 Db 1 TCAAACTGACATCCACACGACAGACAAACACACAGAGAGGCCCT 46
 RESULT 19
 ABL56734
 ID ABL56734 standard; DNA: 41 BP.
 XX
 AC ABL56734;
 XX

PF	30-JUL-2002	(first entry)
XX		
DE	Probe #2 for kruppel zinc finger related protein 70.84 cDNA.	
XX		
KW	Human: kruppel zinc finger related protein 70.84; tumour;	
KW	haemal disorder; HIV infection; immunological disease; inflammation;	
XX	gene therapy; probe; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200226807-A1.	
XX		
PD	04-APR-2002.	
XX		
PF	02-JUL-2001; 2001WO-CN01114.	
XX		
PR	07-JUL-2000; 2000CN-0117012.	
XX		
PA	(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.	
XX		
PI	Mao Y, Xie Y;	
XX		
DR	WPI; 2002-292482/33.	
XX		
PT	Human Kruppel Zinc Finger related protein 70.84 and encoding	
PT	polynucleotide, useful in the diagnosis and treatment of malignant	
PT	tumours, haemal disorders, human immunodeficiency virus infection,	
PT	immunological diseases and inflammation -	
XX		
PS	Example 7; Page 15; 39pp; Chinese.	
XX		
CC	Probes ABL56733-34 were used to identify cDNA encoding a human	
CC	kruppel zinc finger related protein 70.84. The polypeptide and its	
CC	encoding polynucleotide are used in diagnosis and treatment of	
CC	malignant tumour, haemal disorders, human immunodeficiency virus (HIV)	
CC	infection, immunological diseases and various inflammations. The	
CC	polynucleotide may also be used for gene therapy.	
XX		
SO	Sequence 41 BP; 8 A; 9 C; 12 G; 12 T; 0 other;	
	Query Match	1.0%; Score 26.6; DB 24; Length 41;
	Best Local Similarity	78.0%; Pred. No. 4e+02;
	Matches	32; Conservative 0; Mismatches 9; Indels 0; Gaps
OY	301	TGCTGAGACTTATACATCTGTGCTCACTGGAATTC
		1 TGCTGAGAAATTTATGGAAATCTGCGCTCCTCGCAATTC
DB		41
	RESULT 20	
	AAS18906	
ID	AAS18906 standard; DNA; 41 BP.	
XX		
AC	AAS18906;	
XX		
DT	26-MAR-2002 (first entry)	
XX		
DE	Human OZF gene related protein 13 oligonucleotide probe #1.	
XX		
KW	Human: ss: OZF gene related protein 13; cancer; HIV infection;	
XX	human immunodeficiency virus; probe.	
XX		
OS	Homo sapiens.	
XX		
PN	CN1315334-A.	
XX		
PD	03-OCT-2001.	
XX		
PF	27-MAR-2000; 2000CN-0115166.	
XX		
PR	27-MAR-2000; 2000CN-0115166.	
XX		
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.	


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DE 2if-1 specific sense oligo used to generate three finger ZFP.
XX
XX DNA binding protein; zinc finger domain 1; zinc finger protein; ZFP;
KW viral replication; gene expression; virucide; 2if1; ss.
XX
XX Unidentified.
OS
XX
XX WO200208286-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-EP08367.
XX
XX 21-JUL-2000; 2000US-220060P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Sera T;
XX
XX WPI: 2002-172000/22.
XX
XX New Zinc Finger Protein (ZFP) comprising three essential domains useful
XX for diagnosing diseases associated with abnormal genomic structure -
XX
XX Example 7; Page 71; 143pp; English.
XX
XX The present invention relates to novel DNA binding proteins comprising
XX zinc finger domains in which two histidine and two cysteine residues
XX coordinate a central zinc ion. The invention particularly relates to
XX the identification of a context-independent recognition code to design
XX zinc finger domains. The invention also relates to zinc finger proteins
XX (ZFP) designed using this recognition code. The ZFPs are useful for
XX altering genomic structure, inhibiting viral replication (where viral
XX replication is inhibited for plant virus, an animal virus or a human
XX virus), modulating gene expression, detecting an altered zinc finger
XX recognition sequence and diagnosing disease associated with abnormal
XX genomic structure. The present DNA sequence is zinc finger domain 1
XX (2if-1) specific oligonucleotide which is used to generate three finger
XX ZFP for the 11 site of beet curly top virus (BCTV). This sequence is
XX used in the exemplification of the invention.
XX
XX Sequence 60 BP; 18 A; 9 C; 19 G; 14 T; 0 other;
XX
XX
XX Query Match 0.9%; Score 25.8; DB 24; Length 60;
XX Best Local Similarity 73.3%; Pred. No. 9.2e+02;
XX Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX 1593 GGGGAGAACCCATTGTATGTCGAGTCGCGGAGCGCTTACC 1637
XX
XX 1 GGGGAGAACCCGCTATTAATGTCGGAATGTGTAAAGCTTTAGC 45
XX
XX
XX RESULT 26
XX AAD33618
XX ID AAD33618 standard; DNA: 56 BP.
XX
XX AAD33618;
XX
XX 01-JUL-2002 (first entry)
XX
XX 2if-3 specific PCR primer 5 used to generate three finger ZFP.
XX
XX DNA binding protein; zinc finger domain 3; zinc finger protein; ZFP;
KW viral replication; gene expression; virucide; 2if3; PCR; primer; ss.
XX
XX Unidentified.
OS
XX
XX WO200208286-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-EP08367.
XX

```

```

PR 21-JUL-2000; 2000US-220060P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Sera T;
XX
XX WPI: 2002-172000/22.
XX
XX New Zinc Finger Protein (ZFP) comprising three essential domains useful
XX for diagnosing diseases associated with abnormal genomic structure -
XX
XX Example 6; Page 71; 143pp; English.
XX
XX The present invention relates to novel DNA binding proteins comprising
XX zinc finger domains in which two histidine and two cysteine residues
XX coordinate a central zinc ion. The invention particularly relates to
XX the identification of a context-independent recognition code to design
XX zinc finger domains. The invention also relates to zinc finger proteins
XX (ZFP) designed using this recognition code. The ZFPs are useful for
XX altering genomic structure, inhibiting viral replication (where viral
XX replication is inhibited for plant virus, an animal virus or a human
XX virus), modulating gene expression, detecting an altered zinc finger
XX recognition sequence and diagnosing disease associated with abnormal
XX genomic structure. The present DNA sequence is zinc finger domain 3
XX (2if-3) specific PCR primer 5 used to generate three finger ZFP. This
XX sequence is used in the exemplification of the invention.
XX
XX Sequence 56 BP; 13 A; 9 C; 16 G; 10 T; 8 other;
XX
XX
XX Query Match 0.9%; Score 25.6; DB 24; Length 56;
XX Best Local Similarity 72.1%; Pred. No. 1e+03;
XX Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX 1179 AAGCCTTATGTCGCAAGCATGTGCGGAGACCTTACCTCA 1221
XX
XX 7 AAGCCTTACCAAGTGCCCTGAATGCGGAAGACCTTACTNNNA 49
XX
XX
XX RESULT 27
XX ABN34081
XX ID ABN34081 standard; DNA: 60 BP.
XX
XX ABN34081;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:6629.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX
XX 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI: 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes
XX

```


CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 60 BP; 17 A; 13 C; 14 G; 16 T; 0 other;
Query Match 0.9%; Score 25.2; DB 24; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
OY 1225 CAACCTCATTTACCGACAGGCGGCGCACTGGGGAGAACCTTATGTTTCA 1278
DB 5 CACACCTGACTGACATCAGAGGGTTCATCTGAGAGACGACCTTGCAGATGA 58
RESULT 32
ABN45438
ID ABL45438 standard; DNA; 60 BP.
XX
AC ABL45438;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:18186.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI: 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 18186; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABL27253 to ABL59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 60 BP; 19 A; 16 C; 10 G; 15 T; 0 other;
Query Match 0.9%; Score 25.2; DB 24; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
OY 1192 GCAAGGATGTGGCAGAGCTTTAGCCTGAAGCTAAACCTCATTAACCCACAGA 1245
DB 1 GCAATGACACTGGGAGAAACCTTTCAGTATGATCATTCCTCATCAGTCATCAGA 54
RESULT 33
ABL56733
ID ABL56733 standard; DNA; 41 BP.
XX
AC ABL56733;
XX
DT 30-JUL-2002 (first entry)
XX
DE Probe #1 for kruppel zinc finger related protein 70.84 cDNA.
XX
KW Human; kruppel zinc finger related protein 70.84; tumour;
KW haemal disorder; HIV infection; immunological disease; inflammation;
KW gene therapy; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200226807-A1.
XX
PD 04-APR-2002.
XX
PF 02-JUL-2001; 2001WO-CN01114.
XX
PR 07-JUL-2000; 2000CN-0117012.
XX
PA (BLOW-) BLOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI: 2002-292482/33.
XX
PT Human Kruppel zinc finger related protein 70.84 and encoding
PT polynucleotide, useful in the diagnosis and treatment of malignant
PT tumours, haemal disorders, human immunodeficiency virus infection,
PT immunological diseases and inflammation
XX
PS Example 7; Page 15; 39pp; Chinese.
XX
CC Probes ABL56733-34 were used to identify cDNA encoding a human
CC kruppel zinc finger related protein 70.84. The polypeptide and its
CC encoding polynucleotide are used in diagnosis and treatment of
CC malignant tumour, haemal disorders, human immunodeficiency virus (HIV)
CC infection, immunological diseases and various inflammations. The
CC polynucleotide may also be used for gene therapy.
XX
SQ Sequence 41 BP; 8 A; 8 C; 13 G; 12 T; 0 other;
Query Match 0.9%; Score 25; DB 24; Length 41;
Best Local Similarity 75.6%; Pred. No. 1.3e+03;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 301 TGCCTGAGACTTATTAACCATCTGCTGCTGCTGGAATTCCA 341
DB 1 TGCCTGAGAAATTATGGAATGTGGCTCCCTGGGATTCCA 41
RESULT 34
AAS18907
ID AAS18907 standard; DNA; 41 BP.
XX

AC	AAS18907;
XX	
DF	26-MAR-2002 (first entry)
XX	
DE	Human OZF gene related protein 13 oligonucleotide probe #2.
XX	
KW	Human; ss; OZF gene related protein 13; cancer; HIV infection;
KW	human immunodeficiency virus; probe.
XX	
OS	Homo sapiens.
XX	
PN	CN1315334-A.
XX	
PD	03-OCT-2001.
XX	
PF	27-MAR-2000; 2000CN-0115166.
XX	
PR	27-MAR-2000; 2000CN-0115166.
XX	
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX	
PI	Mao Y, Xie Y;
XX	
DR	WPI: 2002-056303/08.
XX	
PT	Polypeptide-OZF gene related protein 13 and polynucleotide encoding
PT	it -
XX	
PS	Example 7; Page 20; 31pp; Chinese.
XX	
CC	The invention relates to a new polypeptide-OZF (not defined) gene related
CC	protein 13, the polynucleotide encoding it, the process for preparing the
CC	said polypeptide by DNA recombination, the application of said
CC	polypeptide in treating several diseases such as cancer and HIV infection
CC	(human immunodeficiency virus). The antagonist against the said
CC	polypeptide and its therapeutic action, and the application of said
CC	polynucleotide for coding this new-OZF correlated protein 13 are
CC	disclosed. The present sequence is an oligonucleotide probe used to
CC	detect nucleic acids encoding OZF gene related protein 13.
XX	
SQ	Sequence 41 BP; 14 A; 7 C; 11 G; 9 T; 0 other;
	Query Match 0.9%; Score 25; DB 24; Length 41;
	Best Local Similarity 75.6%; Pred. No. 1.3e+03;
	Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0
QY	1411 TAAGACACACACAGAGAAGACCTTGTATGCACGAA 1451
Db	1 TGACAAGTCACACACAGGTGACGACCCTTGTTATGTAATGA 41
RESULT 35	
ABN33912	
ID	ABN33912 standard; DNA: 60 BP.
XX	
AC	ABN33912:
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Human spliced transcript detection oligonucleotide SEQ ID NO:6660.
XX	
KM	Human; mouse; rat; splice transcript; detection; RNA transcript;
XX	splice variant; transcriptome; oligonucleotide library; ss.
OS	Homo sapiens.
XX	
PN	N0200210449-A2.
XX	
PD	07-FEB-2002.
XX	
PF	20-JUL-2001; 2001WO-IB01903.
XX	
R	28-JUL-2000; 2000US-221607P.

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PR 02-MAY-2001; 2001US-287724P.
XX (COMP-) COMPUGEN INC.
PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1: SEQ ID 6660; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition, to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 18 A; 15 C; 15 G; 12 T; 0 other;
XX
XX Query Match 0.9%; Score 24.8; DB 24; Length 60;
XX Best Local Similarity 63.3%; Pred. No. 1.9e+03;
XX Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
XX
XX 1033 GTGGGCGACGGCTTACGTGGAAGTCAACACCTGATCACAACATCAGAGGACACACTGAGGG 109
XX 1 GTGGCAAAAGCTTTGGAAGGACACTCCATCTAAGCAACATCAGCGATTTCACACAGGCG 60
XX
XX RESULT 36
XX ABN33916
XX ID ABN33916 standard; DNA; 60 BP.
XX
XX ABN33916;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:6664.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001MO-IB01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX

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PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1; SEQ ID 6664; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 24 A; 8 C; 12 G; 16 T; 0 other:
SO
XX
XX Query Match 0.9%; Score 24.8; DB 24; Length 60;
XX Best Local Similarity 63.3%; Pred. No. 1.9e+03;
XX Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 1659 CACCAAGAGACACACTCAGGAGAGACATTGTGTGTGCTGAGTGGACGAGGCTT 1718
DB 1 CATCAGATTACCCACTTAGAAGAGAACAAATGTAATGTGATGTATGCGAAGCTATTT 60
RESULT 37
ABN34111
ID ABN34111 standard; DNA: 60 BP.
XX
XX ABN34111;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:6859.
DE
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX WO200210449-A2.
FN
XX 07-FEB-2002.
PD
XX 20-JUL-2001; 2001WO-IB01903.
PF
XX 28-JUL-2000; 2000US-221607P.
PR

PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1; SEQ ID 6859; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 13 A; 14 C; 18 G; 15 T; 0 other:
SO
XX
XX Query Match 0.9%; Score 24.8; DB 24; Length 60;
XX Best Local Similarity 67.3%; Pred. No. 1.9e+03;
XX Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
OY 204 GAGCGCTTCGTCGATTCAGGAGATGCTGTGTAATTCACCCAGAGAGACT 255
DB 9 GAGCAATTTGTGACCCCTCAAGAGATGCGCATGACCTTCACCTTGAGAGACT 60
RESULT 38
ABA03751
ID ABA03751 standard; DNA: 41 BP.
XX
XX ABA03751;
XX
XX 18-FEB-2002 (first entry)
XX
XX Human zinc finger protein 22 DNA probe 1.
DE
XX Human; zinc finger protein 22; cancer; nosohaemia; infection;
KW HIV; human immunodeficiency virus; immunological disease;
KW inflammatory disorder; probe; ss.
XX
XX Homo sapiens.
OS
XX CN1307039-A.
FN
XX 08-AUG-2001.
PD
XX 26-JAN-2000; 2000CN-0111545.
PF
XX

PR 26-JAN-2000; 2000CN-0111545.
XX
XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
XX WPI; 2002-062741/09.
XX
XX Polypeptide-human zinc finger protein 22 and polynucleotide for coding
XX said polypeptide -
XX
XX Example 7; Page 20 (disclosure); 34pp; Chinese.
XX
XX The invention relates to a novel polypeptide, human zinc finger protein
CC 22. The polypeptide is useful for treating various diseases, such as
CC malignant tumours, nosohaemia, HIV infection, immunological diseases and
CC inflammatory disorder. The present sequence is a probe used to
CC detect polynucleotides encoding the polypeptide of the invention.
XX
SQ Sequence 41 BP; 17 A; 8 C; 11 G; 5 T; 0 other; .

Query Match 0.9%; Score 24.6; DB 24; Length 41;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1066 TCACACATCAGAGGACACACCTGCGGAGAACCTTATG 1104
DB 1 TGAGACATCAGAGAGTGCACACAGAGAGAAACCTTACG 39

RESULT 39
ABA03752
ID ABA03752 standard; DNA; 41 BP.
XX
XX ABA03752;
XX
XX 18-FEB-2002 (first entry)
XX
XX Human zinc finger protein 22 DNA probe 2.
DE
XX
XX Human; zinc finger protein 22; cancer; nosohaemia; infection;
KW HIV; human immunodeficiency virus; immunological disease;
KW Inflammatory disorder; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX CN1307039-A.
XX
XX 08-AUG-2001.
XX
XX 26-JAN-2000; 2000CN-0111545.
XX
XX 26-JAN-2000; 2000CN-0111545.
XX
XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-062741/09.
XX
XX Polypeptide-human zinc finger protein 22 and polynucleotide for coding
XX said polypeptide -
XX
XX Example 7; Page 20 (disclosure); 34pp; Chinese.
XX
XX The invention relates to a novel polypeptide, human zinc finger protein
CC 22. The polypeptide is useful for treating various diseases, such as
CC malignant tumours, nosohaemia, HIV infection, immunological diseases and
CC inflammatory disorder. The present sequence is a probe used to
CC detect polynucleotides encoding the polypeptide of the invention.
XX
SQ Sequence 41 BP; 16 A; 9 C; 11 G; 5 T; 0 other;

Query Match 0.9%; Score 24.6; DB 24; Length 41;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1066 TCACACATCAGAGGACACACCTGCGGAGAACCTTATG 1104
DB 1 TGAGACATCAGAGAGTGCACACAGAGAGAAACCTTACG 39

RESULT 40
AAH89252
ID AAH89252 standard; DNA; 51 BP.
XX
XX AAH89252;
XX
XX 01-OCT-2001 (first entry)
XX
XX Human transcription factor DNA polymorphic site SEQ ID NO: 33.
DE
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200151670-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US00322.
XX
XX 07-JAN-2000; 2000US-0174962.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach MD;
XX
XX WPI; 2001-451871/48.
XX
XX P-PSDB; AAM00143.
XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX infection and diabetes -
XX
XX Claim 1; Page 119; 475pp; English.
XX
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention.
XX
SQ Sequence 51 BP; 13 A; 10 C; 16 G; 12 T; 0 other;

Query Match 0.9%; Score 24.6; DB 22; Length 51;
Best Local Similarity 70.2%; Pred. No. 2e+03;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1251 CACACTGGGAGAACCTTATGTTTGCAGGGAATGTGGCGTGGCTT 1297
DB 4 CACACTGGAGAGAAACCTTATGATGTTTGCATGTGGAGGACCTT 50

RESULT 41
AAH89253
ID AAH89253 standard; DNA; 51 BP.
XX
XX AAH89253;
XX

```
XX 01-OCT-2001 (first entry)
DT
XX
DE Human transcription factor DNA polymorphic site SEQ ID NO: 34.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KM forensic test; aberrant protein expression; ds.
XX
XX Homo sapiens.
OS
XX WO200151670-A2.
XX
XX 19-JUL-2001.
PD
XX
PF 05-JAN-2001; 2001WO-US00322.
XX
PR 07-JAN-2000; 2000US-0174962.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shinkets RA, Leach MD;
PI
XX WPI; 2001-451871/48.
XX
XX P-PSDB; AAM00144.
DR
XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
XX
XX
XX Claim 1; Page 119; 475pp; English.
PS
XX
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention.
XX
XX
XX Sequence 51 BP; 14 A; 10 C; 15 G; 12 T; 0 other;
SQ
Query Match 0.9%; Score 24.6; DB 22; Length 51;
Best Local Similarity 70.2%; Pred. No. 2e+03;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Oy 1251 CACACTGGGAGAGACCTTATGTTGGCAGGAGATGCGCGTCTT 1297
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 CACACTGGAGAGAAACCTATATATGTTGTGATGTGGAGAGCCCTT 50
RESULT 42
AAD33628/C
ID AAD33628 standard; DNA: 55 BP.
XX
XX AAD33628;
AC
XX
XX 01-JUL-2002 (first entry)
DT
XX
XX Zif-3 specific antisense oligo used to generate three finger ZFP.
DE
XX
XX DNA binding protein; zinc finger domain 3; zinc finger protein; ZFP;
KM viral replication; gene expression; virucide; zif3; ss.
XX
XX Unidentified.
OS
XX WO200208286-A2.
XX
XX 31-JAN-2002.
PD
XX
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PF 19-JUL-2001; 2001WO-EP08367.
XX
XX 21-JUL-2000; 2000US-220060P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Sera T;
PI
XX
XX WPI; 2002-172000/22.
DR
XX
XX New zinc Finger Protein (ZFP) comprising three essential domains useful
PT for diagnosing diseases associated with abnormal genomic structure -
PT
XX
XX Example 7; Page 72; 143pp; English.
PS
XX
XX The present invention relates to novel DNA binding proteins comprising
CC zinc finger domains in which two histidine and two cysteine residues
CC coordinate a central zinc ion. The invention particularly relates to
CC the identification of a context-independent recognition code to design
CC zinc finger domains. The invention also relates to zinc finger proteins
CC (ZFP) designed using this recognition code. The ZFPs are useful for
CC altering genomic structure, inhibiting viral replication (where viral
CC replication is inhibited for plant virus, an animal virus or a human
CC virus), modulating gene expression, detecting an altered zinc finger
CC recognition sequence and diagnosing disease associated with abnormal
CC genomic structure. The present DNA sequence is zinc finger domain 3
CC (Zif-3) specific oligonucleotide which is used to generate three finger
CC ZFP for the LI site of beet curly top virus (BCRV). This sequence is
CC used in the exemplification of the invention.
XX
XX
XX Sequence 55 BP; 9 A; 14 C; 15 G; 17 T; 0 other;
SQ
Query Match 0.9%; Score 24.6; DB 24; Length 55;
Best Local Similarity 65.5%; Pred. No. 2.1e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Oy 1211 CTTAGCCTGAGTCAACCTATTACCCAGAGGCGGACACTGGGAGAG 1265
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 55 CTTAGTCGTGTGATGATGATCAACACCCAGCAGCAGCAGCGGAGAG 1
RESULT 43
ABN34011
ID ABN34011 standard; DNA: 60 BP.
XX
XX ABN34011;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:6759.
DE
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX WO200210449-A2.
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IB01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX
XX 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
```

PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes

XX Example 1: SEQ ID 6759; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting RNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition: to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences).

SQ Sequence 60 BP; 20 A; 17 C; 9 G; 14 T; 0 other;

Query Match 0.9%; Score 24.6; DB 24; Length 60;
Best Local Similarity 65.5%; Pred. No. 2.2e+03;

Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1375 AAGCGTTTGAAGAGAGTGCACACCTCATGACACTTAAAGACACACAGAGCA 1429
DB 5 AAGTCTTGAGCCATCATCTCATCCCTTAACAGGACACTTGAATCTTACACGACAGA 59

RESULT 44

AL332659
ID AAL32659 standard; DNA; 51 BP.

AC AAL32659;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #5867.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

XX Homo sapiens.

OS WO200147944-A2.

PN 05-JUL-2001.

PD 28-DEC-2000; 2000WO-US35498.

PF 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections.

PS Claim 1: Page 3073; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. Rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

SQ Sequence 51 BP; 15 A; 6 C; 14 G; 16 T; 0 other;

Query Match 0.9%; Score 24.4; DB 22; Length 51;
Best Local Similarity 68.0%; Pred. No. 2.3e+03;

Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1353 TACATTGACGAGGTGTGAGCAAGGCTTTAGCAGAACTCACACCTCAT 1402
DB 1 TATAATGTGATGAGTGTGAGCAAGGCTTCACTGACAGCTCAGATCTTAT 50

RESULT 45

AL333200
ID AAL33200 standard; DNA; 51 BP.

AC AAL33200;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #6408.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

XX Homo sapiens.

OS WO200147944-A2.

PN 05-JUL-2001.

PD 28-DEC-2000; 2000WO-US35498.

PF 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-465210/50.

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 05:33:54 ; Search time 7121 Seconds

(without alignments)
11328.883 Million cell updates/sec

Title: US-09-898-556a-3

Perfect score: 2772

Sequence: 1 cagcgcgcttaagctgctggtg.....ttctaccatccctaccct 2772

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 897812

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	49.4	1.8	51.6	AX165270	AX165270 Sequence
C 2	49.4	1.8	51.6	AX165674	AX165674 Sequence
C 3	34.6	1.2	51.6	AX161256	AX161256 Sequence
C 4	33	1.2	51.6	AX161255	AX161255 Sequence
C 5	27.8	1.0	51.6	AX163066	AX163066 Sequence
C 6	27.6	1.0	51.6	AX161706	AX161706 Sequence
C 7	27	1.0	60.6	AX382506	AX382506 Sequence
C 8	26.6	1.0	51.6	AX199456	AX199456 Sequence
C 9	26.6	1.0	56.6	AX382519	AX382519 Sequence
C 10	26.2	0.9	51.6	AX163065	AX163065 Sequence
C 11	26	0.9	51.6	AX161705	AX161705 Sequence
C 12	25.8	0.9	60.6	AX382515	AX382515 Sequence
C 13	25.6	0.9	56.6	AX382518	AX382518 Sequence
C 14	24.6	0.9	51.6	AX199103	AX199103 Sequence
C 15	24.6	0.9	51.6	AX199104	AX199104 Sequence
C 16	24.6	0.9	55.6	AX382520	AX382520 Sequence
C 17	23.8	0.9	51.6	AX163385	AX163385 Sequence
C 18	23.8	0.9	55.6	AX382511	AX382511 Sequence
C 19	23	0.8	51.6	AX159659	AX159659 Sequence
C 20	23	0.8	51.6	AX199545	AX199545 Sequence
C 21	23	0.8	60.6	AX449256	AX449256 Sequence
C 22	22.4	0.8	48.6	HUM2NF	M8369 Homo sapien
C 23	22.4	0.8	60.6	AX382509	AX382509 Sequence
C 24	22.4	0.8	60.6	AX382518	AX382518 Sequence
C 25	22.2	0.8	51.6	AX163386	AX163386 Sequence
C 26	21.8	0.8	51.6	AX115765	AX115765 Sequence
C 27	21.6	0.8	41.6	AR036764	AR036764 Sequence
C 28	21.6	0.8	60.6	AF062523	AF062523 Mus muscu
C 29	21.4	0.8	51.6	AX159660	AX159660 Sequence
C 30	21.4	0.8	60.6	AX449255	AX449255 Sequence
C 31	21.2	0.8	50.6	AX158732	AX158732 Sequence
C 32	21.2	0.8	59.6	HSADD2S16	AF000096 Homo sapi
C 33	21	0.8	31.6	AX249323	AX249323 Sequence
C 34	21	0.8	45.6	AX382526	AX382526 Sequence
C 35	21	0.8	48.6	A84824	A84824 Sequence 19
C 36	21	0.8	50.6	AR107677	AR107677 Sequence
C 37	21	0.8	52.6	AR168446	AR168446 Sequence
C 38	21	0.8	59.6	AR165671	AR165671 Sequence
C 39	20.8	0.8	48.6	A42976	A42976 Sequence 11
C 40	20.8	0.8	48.6	A45522	A45522 Sequence 7
C 41	20.8	0.8	48.6	AR030794	AR030794 Sequence
C 42	20.8	0.8	48.6	AR082131	AR082131 Sequence
C 43	20.8	0.8	51.6	AX165344	AX165344 Sequence
C 44	20.6	0.7	51.6	AX162153	AX162153 Sequence
C 45	20.6	0.7	51.6	AX162154	AX162154 Sequence
C 46	20.6	0.7	52.6	AR165679	AR165679 Sequence
C 47	20.6	0.7	60.6	HUMNMIE1E	L05010 Homo sapien
C 48	20.4	0.7	51.6	AX158272	AX158272 Sequence
C 49	20.4	0.7	52.10	D50270	D50270 Mouse Pig-f
C 50	20.2	0.7	50.6	AR040811	AR040811 Sequence
C 51	20.2	0.7	52.6	A41832	A41832 Sequence 13
C 52	20.2	0.7	53.6	I24813	I24813 Sequence 2
C 53	20.2	0.7	57.9	S57604	S57604 T-cell - rece
C 54	20.2	0.7	60.6	AX429005	AX429005 Sequence
C 55	20.2	0.7	60.6	I42389	I42389 Sequence 21
C 56	20	0.7	31.6	AX249325	AX249325 Sequence
C 57	20	0.7	48.6	AR000192	AR000192 Sequence
C 58	20	0.7	48.6	AX008144	AX008144 Sequence
C 59	20	0.7	50.6	AX395011	AX395011 Sequence
C 60	20	0.7	52.6	AX184291	AX184291 Sequence
C 61	20	0.7	55.6	AR112996	AR112996 Sequence
C 62	20	0.7	55.6	E49740	E49740 Biological
C 63	20	0.7	55.6	I28996	I28996 Sequence 7
C 64	20	0.7	56.6	AX008143	AX008143 Sequence
C 65	19.8	0.7	47.6	AR110217	AR110217 Sequence

C 66	19.8	0.7	47	6	AR169976	Sequence	C 139	19	0.7	51	6	AX158371	AX158371	Sequence
C 67	19.8	0.7	47	6	AR171785	Sequence	C 140	19	0.7	51	6	AX160377	AX160377	Sequence
C 68	19.8	0.7	47	6	AX378376	Sequence	C 141	19	0.7	51	6	AX162285	AX162285	Sequence
C 69	19.8	0.7	47	6	BD009010	Promoter	C 142	19	0.7	51	6	AX163319	AX163319	Sequence
C 70	19.8	0.7	50	6	AX159884	Sequence	C 143	19	0.7	51	6	AX165251	AX165251	Sequence
C 71	19.8	0.7	51	6	AX158137	Sequence	C 144	19	0.7	51	6	AX204116	AX204116	Sequence
C 72	19.8	0.7	51	6	AX159652	Sequence	C 145	19	0.7	52	8	CNS01BxV	AL114827	Botrytis
C 73	19.8	0.7	51	6	AX160179	Sequence	C 146	19	0.7	54	6	A13518	A13518	DNA fragment
C 74	19.8	0.7	51	6	AX165672	Sequence	C 147	19	0.7	54	6	A52692	A52692	Human
C 75	19.8	0.7	57	3	AB032141	Drosophila	C 148	19	0.7	54	9	HUMG2A03	M10798	Human alpha
C 76	19.8	0.7	57	3	AR117908	Sequence	C 149	19	0.7	57	6	A41144	A41144	Sequence 41
C 77	19.8	0.7	59	6	AX286580	Sequence	C 150	19	0.7	57	6	AR153765	AR153765	Sequence
C 78	19.6	0.7	48	6	AX047705	Sequence	C 151	19	0.7	57	9	MTSLA576	X89640	H. sapiens m
C 79	19.6	0.7	51	6	AX117637	Sequence	C 152	19	0.7	59	6	AX011337	AX011337	Sequence
C 80	19.6	0.7	51	6	AX117789	Sequence	C 153	19	0.7	60	10	AF328233	AF328233	Mus muscu
C 81	19.6	0.7	51	6	AX117861	Sequence	C 154	18.8	0.7	40	6	AX079225	AX079225	Sequence
C 82	19.6	0.7	51	6	AX157005	Sequence	C 155	18.8	0.7	40	6	AX080067	AX080067	Sequence
C 83	19.6	0.7	51	6	AX157006	Sequence	C 156	18.8	0.7	43	6	AR013755	AR013755	Sequence
C 84	19.6	0.7	51	6	AX161747	Sequence	C 157	18.8	0.7	43	6	AR013756	AR013756	Sequence
C 85	19.6	0.7	51	6	AX190113	Sequence	C 158	18.8	0.7	49	6	AR011505	AR011505	Sequence
C 86	19.6	0.7	53	6	I05885	Sequence 2	C 159	18.8	0.7	49	6	AR061800	I18143	Sequence 7
C 87	19.6	0.7	53	6	I05930	Sequence 2	C 160	18.8	0.7	50	6	AX093090	I18143	Sequence 37
C 88	19.6	0.7	53	6	I08801	Sequence 1	C 161	18.8	0.7	50	6	AX093090	AX093090	Sequence
C 89	19.6	0.7	53	6	I09164	Sequence 2	C 162	18.8	0.7	50	6	AX161748	AX161748	Sequence
C 90	19.6	0.7	55	6	I09610	Sequence 1	C 163	18.8	0.7	51	6	AX158271	AX158271	Sequence
C 91	19.6	0.7	56	6	I43365	Sequence 9	C 164	18.8	0.7	51	6	AX158899	AX158899	Sequence
C 92	19.6	0.7	56	6	I61420	Sequence 9	C 165	18.8	0.7	51	6	AX160140	AX160140	Sequence
C 93	19.6	0.7	56	6	I66034	Sequence 9	C 166	18.8	0.7	51	6	AX160496	AX160496	Sequence
C 94	19.6	0.7	57	3	S59976	TAL1d2-prot	C 167	18.8	0.7	51	6	AX199398	AX199398	Sequence
C 95	19.6	0.7	59	3	AF411985	Formica e	C 168	18.8	0.7	51	6	AX204439	AX204439	Sequence
C 96	19.6	0.7	59	3	I09611	Sequence 2	C 169	18.8	0.7	51	6	AX304454	AX304454	Sequence
C 97	19.6	0.7	59	6	S43435S10	transmembr	C 170	18.8	0.7	54	6	A22726	A22726	synthetic f
C 98	19.6	0.7	60	6	AR163465	Sequence	C 171	18.8	0.7	54	6	A47685	A47685	Sequence 3
C 99	19.6	0.7	60	6	AR163466	Sequence	C 172	18.8	0.7	54	6	AX135220	AX135220	Sequence
C 100	19.4	0.7	33	6	BD010994	HIV probe	C 173	18.8	0.7	54	6	BD006609	BD006609	Process f
C 101	19.4	0.7	45	6	AX382524	Sequence	C 174	18.8	0.7	54	6	I07497	I07497	Sequence 3
C 102	19.4	0.7	48	10	MUSIGHZ	Mouse Ig ge	C 175	18.8	0.7	54	6	I21368	I21368	Sequence 6
C 103	19.4	0.7	50	6	AX159889	Sequence	C 176	18.8	0.7	54	9	HSTCEL16	X81551	H. sapiens r
C 104	19.4	0.7	50	10	PF246197SO2	Rattus no	C 177	18.8	0.7	56	6	AX061289	AX061289	Sequence
C 105	19.4	0.7	51	6	AX156932	Sequence	C 178	18.8	0.7	59	3	AF411985	AF411985	Formica e
C 106	19.4	0.7	51	6	AX162214	Sequence	C 179	18.8	0.7	59	6	AX150275	AX150275	Sequence
C 107	19.4	0.7	51	6	AX204400	Sequence	C 180	18.8	0.7	60	9	HUMSAU3A04	HUMSAU3A04	Human alpha
C 108	19.4	0.7	55	9	S76405	Sequence	C 181	18.8	0.7	60	9	HUMSAU3A61	HUMSAU3A61	Human alpha
C 109	19.4	0.7	57	9	AF011607	Homo sapi.	C 182	18.6	0.7	25	6	AR207599	AR207599	Sequence
C 110	19.4	0.7	57	9	AF011639	Homo sapi.	C 183	18.6	0.7	25	6	E50868	E50868	Gene inhibi
C 111	19.4	0.7	59	6	A84789	Sequence 34	C 184	18.6	0.7	36	6	AR041498	AR041498	Sequence
C 112	19.2	0.7	41	6	A58755	Sequence 1	C 185	18.6	0.7	36	9	S59762	S59762	IgVH-pre-B-
C 113	19.2	0.7	44	6	AR118799	Sequence	C 186	18.6	0.7	38	6	AR159578	AR159578	Sequence
C 114	19.2	0.7	45	6	AR032488	Sequence	C 187	18.6	0.7	39	6	A70765	A70765	Sequence 86
C 115	19.2	0.7	45	6	AR209152	Sequence	C 188	18.6	0.7	39	6	A79249	A79249	Sequence 86
C 116	19.2	0.7	45	6	I29228	Sequence 10	C 189	18.6	0.7	39	6	BD003479	BD003479	A gene re
C 117	19.2	0.7	45	6	I90902	Sequence 10	C 190	18.6	0.7	42	6	AR031386	AR031386	Sequence
C 118	19.2	0.7	48	6	AR176079	Sequence	C 191	18.6	0.7	42	6	BD009754	BD009754	Compositi
C 119	19.2	0.7	50	9	AF156531	Homo sapi	C 192	18.6	0.7	43	6	AX010673	AX010673	Sequence
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C 125	19.2	0.7	57	9	HSN224240	Homo sapi	C 198	18.6	0.7	47	6	AR126937	AR126937	Sequence
C 126	19.2	0.7	58	6	AR061277	Sequence	C 199	18.6	0.7	48	6	I15842	I15842	Sequence 16
C 127	19.2	0.7	59	6	AR125099	Sequence	C 200	18.6	0.7	48	10	AB001352	AB001352	Mus muscu
C 128	19.2	0.7	30	6	AX057116	Sequence	C 201	18.6	0.7	50	6	AX160044	AX160044	Sequence
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C 130	19	0.7	35	6	E32613	Novel nucle	C 203	18.6	0.7	51	6	AX115045	AX115045	Sequence
C 131	19	0.7	38	6	AR045392	Sequence	C 204	18.6	0.7	51	6	AX157068	AX157068	Sequence
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ALIGNMENTS

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RESULT 1
AXI65270/c
LOCUS AXI65270 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 465 from Patent WO0138586.
ACCESSION AXI65270
VERSION AXI65270.1 GI:14546099
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 465 31-MAY-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
variation 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
26
/note="single nucleotide polymorphism
Accession number C943297259"
BASE COUNT 9 a 10 c 14 g 18 t
ORIGIN
Query Match 1.8%; Score 49.4; DB 6; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.002;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1378 GCTTAGCCAGAGTCACACCTCATCAGACTTAAGCAGACACAGAG 1428
DB 51 GCTTAGCCAGAGTCACACCTCATCAGACTTAAGCAGACACAGAG 1

RESULT 2
AXI65674/c
LOCUS AXI65674 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 869 from Patent WO0138586.
ACCESSION AXI65674
VERSION AXI65674.1 GI:14546503
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 869 31-MAY-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
variation 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
26
/note="single nucleotide polymorphism
Accession number C943297259"
BASE COUNT 10 a 14 c 12 g 15 t
ORIGIN
Query Match 1.8%; Score 49.4; DB 6; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.002;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1362 AGGAGGTGAGCAGAGCTTATGAGAGTACACACCTCATCAGACTTA 1412
DB 51 AGGAGGTGAGCAGAGCTTATGAGAGTACACACCTCATCAGACTTA 1
```

```
RESULT 3
AXI61256
LOCUS AXI61256 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4584 from Patent WO0140521.
ACCESSION AXI61256
VERSION AXI61256.1 GI:14542587
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4584 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
misc_feature 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
26
/note="2 of 2 allelic variants (4583 is other entry)
Accession number C943960167"
BASE COUNT 17 a 14 c 13 g 7 t
ORIGIN
Query Match 1.2%; Score 34.6; DB 6; Length 51;
Best Local Similarity 81.6%; Pred. No. .78;
Matches 40; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2375 AGTCAAAATGCCAGGACATAGGGGTGAGTACTGTGAACCCAACT 2423
DB 1 AGTCAAAATGCCAGGACATAGGGGTAGGTAGCTGACAGTGAACCCAACT 49

RESULT 4
AXI61255
LOCUS AXI61255 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4583 from Patent WO0140521.
ACCESSION AXI61255
VERSION AXI61255.1 GI:14542586
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4583 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
misc_feature 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
26
/note="1 of 2 allelic variants (4584 is other entry)
Accession number C943960167"
BASE COUNT 17 a 15 c 13 g 6 t
ORIGIN
Query Match 1.2%; Score 33; DB 6; Length 51;
Best Local Similarity 79.6%; Pred. No. 2.5e+02;
Matches 39; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2375 AGTCAAAATGCCAGGACATAGGGGTGAGTACTGTGAACCCAACT 2423
DB 1 AGTCAAAATGCCAGGACATAGGGGTAGGTAGCTGACAGTGAACCCAACT 49
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LOCUS	AXI63066	51 bp	DNA	Linear	PAT 22-JUN-2001
DEFINITION	Sequence 6394 from Patent WO0140521.				
ACCESSION	AXI63066				
VERSION	AXI63066.1	GI:14544397			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 51)				
TITLE	Shimkets, R.A. and Leach, M.				
JOURNAL	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
PATENT	Patent: WO 0140521-A 6394 07-JUN-2001;				
Curagen Corporation (US)					
FEATURES	Location/Qualifiers				
Source	1..51				
misc_feature	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	26				
	/note="2 of 2 allelic variants (6393 is other entry)"				
	Accession number cg4392631"				
BASE COUNT	16 a	6 c	18 g	11 t	
ORIGIN					
Query Match	1.0%: Score 27.8; DB 6; Length 51;				
Best Local Similarity	74.5%: Pred. No.1e+04;				
Matches	35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;				
OY	1243 AGAGGCGGCACACTGGGAGAAAGCTTATGTTGTCAGAGGAATGTGGG 1289				
Db	1 AGAGAGTCCACACTGGAGAGAAAGCTTATAGATGTGTGTGGATGTGGG 47				
RESULT 6					
LOCUS	AXI61706/c	51 bp <td>DNA</td> <td>Linear</td> <td>PAT 22-JUN-2001</td>	DNA	Linear	PAT 22-JUN-2001
DEFINITION	Sequence 5034 from Patent WO0140521.				
ACCESSION	AXI61706				
VERSION	AXI61706.1	GI:14543037			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 51)				
TITLE	Shimkets, R.A. and Leach, M.				
JOURNAL	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
PATENT	Patent: WO 0140521-A 5034 07-JUN-2001;				
Curagen Corporation (US)					
FEATURES	Location/Qualifiers				
Source	1..51				
misc_feature	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	26				
	/note="2 of 2 allelic variants (5033 is other entry)"				
	Accession number cg43981141"				
BASE COUNT	13 a	10 c	13 g	15 t	
ORIGIN					
Query Match	1.0%: Score 27.6; DB 6; Length 51;				
Best Local Similarity	72.0%: Pred. No.1.2e+04;				
Matches	36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;				
OY	1687 CATTGTGATGCTGAGGAGTGAGAGAGCTTATGTAAGTCCACCCCTC 1736				
Db	51 CTTATGATGTACAGAGTGTGGAAAGCCTTCAACATAGTCCACCCCTC 2				

AX382506	LOCUS	AX382506	60 bp	DNA	linear	PAT 18-MAR-2002
DEFINITION	Sequence 36 from Patent WO0208286.					
ACCESSION	AX382506					
VERSION	AX382506.1	GI:19577257				
KEYWORDS						
SOURCE						
ORGANISM	synthetic construct.					
REFERENCE	1	artificial sequences.				
AUTHORS	Sera, T.					
TITLE	zinc finger domain recognition code and uses thereof					
JOURNAL	Patent: WO 0208286-A 36 31-JUN-2002;					
	Syngenta Participations AG (CH)					
FEATURES	Location/Qualifiers					
source	1..60	/organism="synthetic construct"				
		/db_xref="taxon:32630"				
		/note="Partial zinc finger domain oligomer."				
BASE COUNT	15 a 6 c 17 g 13 t	9 others				
ORIGIN						
Query Match	1.0%: Score 27; DB 6; Length 60;					
Best Local Similarity	60.0%: Pred. No. 1.8e+04;					
Matches	36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;					
QY	1593 GGGGAGAGCCATTGTGTATGACGAGTGTGGGAGGCTTTACCGGAAATCAACCTG 1652					
Db	1 GGGGAGAGCCGTTAAATGTCGCGAATGTGTAAAGTTTACGNNNAGCNNNNNTTG 60					
RESULT 8						
LOCUS	AX199456	51 bp	DNA	linear	PAT 29-AUG-2001	
DEFINITION	Sequence 386 from Patent WO0151670.					
ACCESSION	AX199456					
VERSION	AX199456.1	GI:15389859				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 51)					
AUTHORS	Shinketsu, R.A. and Leach, M.D.					
TITLE	Nucleic acids containing single nucleotide polymorphisms and					
	methods of use thereof					
JOURNAL	Patent: WO 0151670-A 386 19-JUL-2001;					
	Curagen Corporation (US)					
FEATURES	Location/Qualifiers					
source	1..51	/organism="Homo sapiens"				
		/db_xref="taxon:9606"				
misc_feature	26	/note="2 of 2 allelic variants (385 is other entry)				
		Accession number c943300708"				
BASE COUNT	6 a 13 c 23 g 9 t					
ORIGIN						
Query Match	1.0%: Score 26.6; DB 6; Length 51;					
Best Local Similarity	71.4%: Pred. No. 2.4e+04;					
Matches	35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;					
QY	1960 GCTTACCGCGAGTACACCTCATTTAGACACGAGAGACATTCAGG 2008					
Db	49 GCTTACCGCGCGCCCTCGCACCTGCTGGCGACACGAGGACTCACACAGG 1					
RESULT 9						
LOCUS	AX382519	56 bp	DNA	linear	PAT 18-MAR-2002	
DEFINITION	Sequence 49 from Patent WO0208286.					
ACCESSION	AX382519					
VERSION	AX382519.1	GI:19577270				

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS Sera, T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 49 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
source
1.56
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial zinc finger domain oligomer."
BASE COUNT 15 a 10 c 19 g 12 t
ORIGIN

Query Match 1.0%; Score 26.6; DB 6; Length 56;
Best Local Similarity 71.4%; Pred. No. 2.4e+04;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 921 GGGGAGACACCTTACATGTACACTGAGTGGGAGACAGCTTGGCAGTA 969
Db 1 GGGGAGAGCCTTACAGTGCCTGAAATCGGAGAGAGCTTATGCTGA 49

RESULT 10
AX163065
LOCUS AX163065 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6393 from Patent WO0140521.
ACCESSION AX163065
VERSION AX163065.1 GI:14544396
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0140521-A 6393 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature
26
/note="1 of 2 allelic variants (6394 is other entry)
Accession number C943926631"
BASE COUNT 16 a 7 c 18 g 10 t
ORIGIN

Query Match 0.9%; Score 26.2; DB 6; Length 51;
Best Local Similarity 72.3%; Pred. No. 3.2e+04;
Matches 34; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1243 AGAGGCGCACACTGGGAGAGCCCTATGTTGCGAGGAATCTGGC 1289
Db 1 AGAGGATCCACACTGGAGAGAAACCTATAGATGTTGGATGTGG 47

RESULT 11
AX161705
LOCUS AX161705 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5033 from Patent WO0140521.
ACCESSION AX161705
VERSION AX161705.1 GI:14543036
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 51)
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5033 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature
26
/note="1 of 2 allelic variants (5034 is other entry)
Accession number C943981141"
BASE COUNT 13 a 11 c 13 g 14 t
ORIGIN

Query Match 0.9%; Score 26; DB 6; Length 51;
Best Local Similarity 70.0%; Pred. No. 3.6e+04;
Matches 35; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1687 CATTGTATGCTGCTGAGTGGAGCAGCGCTTAAATGATAGTCCACCCTC 1736
Db 51 CTTATGATATGATACAGATGTGGAGAGCCCTCAACATATGTCACCCCTC 2

RESULT 12
AX382515
LOCUS AX382515 60 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 45 from Patent WO0208286.
ACCESSION AX382515
VERSION AX382515.1 GI:19577266
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE
1
AUTHORS Sera, T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 45 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
source
1.60
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial zinc finger domain oligomer."
BASE COUNT 18 a 9 c 19 g 14 t
ORIGIN

Query Match 0.9%; Score 25.8; DB 6; Length 60;
Best Local Similarity 73.3%; Pred. No. 4.3e+04;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1593 GGGGAGAGCCATTGTATGTACGAGTGTGGCGAGGCTTACC 1637
Db 1 GGGGAGAGCCGATATAATGTCCGGAATGTGTAAAGATTATAGC 45

RESULT 13
AX382510
LOCUS AX382510 56 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 40 from Patent WO0208286.
ACCESSION AX382510
VERSION AX382510.1 GI:19577261
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE
1
AUTHORS Sera, T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 40 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
Location/Qualifiers

source 1.56
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial zinc finger domain oligomer."
BASE COUNT 13 a 9 c 16 g 10 t 8 others
ORIGIN

Query Match 0.9%; Score 25.6; DB 6; Length 56;
Best Local Similarity 72.1%; Pred. No. 4.9e+04;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1179 AACCTTATGTGCAAGAAATGTGGCAGACCTTACCTGA 1221
1179 AACCTTATGTGCAAGAAATGTGGCAGACCTTACCTGA 1221
7 AACCTTACAGATGCCCTGAATGCGGAGAGACCTTATGNNNA 49

RESULT 14
AX199103
LOCUS AX199103 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 33 from Patent WO0151670.
ACCESSION AX199103
VERSION AX199103.1 GI:15389447
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Shimkets,R.A. and Leach,M.D.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0151670-A 33 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 26
/note="1 of 2 allelic variants (34 is other entry)"
Accession number cg43926631"
BASE COUNT 13 a 10 c 16 g 12 t
ORIGIN

Query Match 0.9%; Score 24.6; DB 6; Length 51;
Best Local Similarity 70.2%; Pred. No. 9.9e+04;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1251 CACACTGGGAGAACCTTATGTTTGCAGGAAATGTGGCGCTT 1297
1251 CACACTGGGAGAACCTTATGTTTGCAGGAAATGTGGCGCTT 1297
4 CACACTGGAGAGAACCTTATGATGTTGTGATGTGGAGGCGCTT 50

RESULT 15
AX199104
LOCUS AX199104 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 34 from Patent WO0151670.
ACCESSION AX199104
VERSION AX199104.1 GI:15389448
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Shimkets,R.A. and Leach,M.D.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0151670-A 34 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 26
/note="2 of 2 allelic variants (33 is other entry)"
Accession number cg43926631"
BASE COUNT 14 a 10 c 15 g 12 t
ORIGIN

Query Match 0.9%; Score 24.6; DB 6; Length 51;
Best Local Similarity 70.2%; Pred. No. 9.9e+04;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1251 CACACTGGGAGAACCTTATGTTTGCAGGAAATGTGGCGCTT 1297
1251 CACACTGGGAGAACCTTATGTTTGCAGGAAATGTGGCGCTT 1297
4 CACACTGGAGAGAACCTTATGATGTTGTGATGTGGAGGCGCTT 50

RESULT 16
AX382520/c
LOCUS AX382520 55 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 50 from Patent WO0208286.
ACCESSION AX382520
VERSION AX382520.1 GI:19577271
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Sera,T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 50 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
source location/Qualifiers
1.55
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial zinc finger domain oligomer."

BASE COUNT 9 a 14 c 15 g 17 t
ORIGIN

Query Match 0.9%; Score 24.6; DB 6; Length 55;
Best Local Similarity 65.5%; Pred. No. 1e+05;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1211 CTTTACCTGAACTCAACCTCATTAACCCACAGAGGCGACACTGGGAGAAG 1265
1211 CTTTACCTGAACTCAACCTCATTAACCCACAGAGGCGACACTGGGAGAAG 1265
55 CTTTACCTGAGATGATAGCTTACCAACCCACAGAGGCGAGGAGAG 1

RESULT 17
AX163385/c
LOCUS AX163385 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6713 from Patent WO0140521.
ACCESSION AX163385
VERSION AX163385.1 GI:14544716
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Shimkets,R.A. and Leach,M.D.
JOURNAL Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0140521-A 6713 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 26
/note="1 of 2 allelic variants (6714 is other entry)"
Accession number cg43280136"
BASE COUNT 15 a 13 c 17 g 6 t
ORIGIN

Query Match 0.9%; Score 23.8; DB 6; Length 51;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2475 CTTCCATTGGTGGTTCCTCCGATGATCCCAACCTTACCTATT 2525
Db 51 CTCCTCGGGCGGTGGGCTCCGATTTCTTCACGCGATGACATATT 1

RESULT 18
AX382511/c 55 bp DNA linear PAT 18-MAR-2002
LOCUS Sequence 41 from Patent WO0208286.

DEFINITION AX382511
ACCESSION AX382511
VERSION AX382511.1 GI:19577262

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

AUTHORS Sera, T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 41 31-JAN-2002;
SYNGENTA PARTICIPATIONS AG (CH)
LOCATION/Qualifiers

FEATURES
source 1.55
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 7 a 11 c 14 t 12 others
ORIGIN

Query Match 0.9%; Score 23.8; DB 6; Length 55;
Best Local Similarity 56.4%; Pred. No. 1.8e+05;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCTGAGTCAACCTTACAAACACAGAGGTACACGCGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACANNNCACCAACGACGACGCGGAGAG 1

RESULT 19
AX159659/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 2987 from Patent WO0140521.

DEFINITION AX159659
ACCESSION AX159659
VERSION AX159659.1 GI:14540990

KEYWORDS human.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2987 07-JUN-2001;
CURAGEN CORPORATION (US)
LOCATION/Qualifiers

FEATURES
source 1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 21 a 9 c 12 g 9 t
ORIGIN

Query Match 0.8%; Score 23; DB 6; Length 51;
Best Local Similarity 74.4%; Pred. No. 3.1e+05;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2723 GAGAGCTGTCTTTTGGCTCAATAAATCTTTTCTACCC 2761
Db 43 GAGCTTCTCTTTTGGCTTATTAACCTCTGTTCCAAAC 5

RESULT 20
AX199545 51 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 475 from Patent WO0151670.

DEFINITION AX199545
ACCESSION AX199545
VERSION AX199545.1 GI:15389970

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide, polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 475 19-JUL-2001;
CURAGEN CORPORATION (US)
LOCATION/Qualifiers

FEATURES
source 1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 13 a 16 c 14 g 8 t
ORIGIN

Query Match 0.8%; Score 23; DB 6; Length 51;
Best Local Similarity 68.1%; Pred. No. 3.1e+05;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1056 TCAACCTGATTCACATCAGAGACACTCAGGAGGAACCTTA 1102
Db 4 TCGATGTGAAGGCGCATCTGCGACGACACAGAGGTAGAAGCCCTA 50

RESULT 21
AX449256 60 bp DNA linear PAT 03-JUL-2002
LOCUS Sequence 34 from Patent WO0206327.

DEFINITION AX449256
ACCESSION AX449256
VERSION AX449256.1 GI:21698014

KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Wang, Z. and Xiao, W.
TITLE A method for prognosing cancer and the proteins involved
JOURNAL Patent: WO 0206327-A 34 24-JAN-2002;
NORTHWESTERN UNIVERSITY (US)
LOCATION/Qualifiers

FEATURES
source 1.60
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 11 a 16 c 17 g 16 t
ORIGIN

Query Match 0.8%; Score 23; DB 6; Length 60;
Best Local Similarity 68.1%; Pred. No. 3.2e+05;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 89 TCAGATCCGGGCGGTGACCCGCTTCATCTGCTTGAGACTT 135
Db 6 TCTGATCCGAGGTGAGTACTGACGCTTACACACCTTCCAGACTT 52

LOCUS	HUM2NZFM	48 bp	DNA	linear	PRI 14-JAN-1995
DEFINITION	Homo sapiens DNA-binding protein (ZNF) gene, partial cds.				
ACCESSION	M88369				
VERSION	M88369.1	GI:340475			
KEYWORDS	DNA-binding protein; zinc finger protein.				
SOURCE	Homo sapiens Placenta DNA.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.				
AUTHORS	Bray, P., Lichter, P., Thiesen, H.J., Ward, D.C. and David, I.B.				
TITLE	Characterization and mapping of human genes encoding zinc finger proteins				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 88 (21), 9563-9567 (1991)				
MEDLINE	92052132				
PUBMED	1946370				
REFERENCE	2 (bases 1 to 48)				
AUTHORS	Lichter, P., Bray, P., Ried, T., David, I.B. and Ward, D.C.				
TITLE	Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile site regions of human chromosomes				
JOURNAL	Genomics 13 (4), 999-1007 (1992)				
MEDLINE	92372070				
PUBMED	1505991				
FEATURES	Location/Qualifiers				
source	1. 48				
gene	/organism="Homo sapiens"				
CDS	/db_xref="taxon:9606"				
	/tissue_type="Placenta"				
	1. 48				
	/gene="ZNF"				
	/partial				
	/gene="ZNF"				
	/strand_name="zinc finger motif"				
	/note="putative"				
	/codon_start=1				
	/product="DNA-binding protein"				
	/protein_id="AAA61327.1"				
	/db_xref="GI:340475"				
	/translation="IHTEGKPSRCRECSKA"				
BASE COUNT	10 a 15 c 17 g 6 t				
ORIGIN					
Query Match	0.8%; Score 22.4; DB 9; Length 48;				
Best Local Similarity	72.5%; Pred. No. 4.7e+05;				
Matches	29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;				
OY	1755 CATTGACGGGAGAAAGCCTTTATGTCACGAGAGTGTGCA	1794			
Db	4 CACACGGGGGAGAAAGCCTTCCTGCGCGAGATGACGA	43			
RESULT 23					
AX382509/c	AX382509	60 bp	DNA	linear	PAT 18-MAR-2002
LOCUS	Sequence 39 from Patent WO0208286.				
DEFINITION	AX382509				
ACCESSION	AX382509				
VERSION	AX382509.1	GI:19577260			
KEYWORDS	synthetic construct.				
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Sera, T.				
TITLE	Zinc finger domain recognition code and uses thereof				
JOURNAL	Patent: WO 0208286-A 39 31-JAN-2002;				
SYNGENTA PARTICIPATIONS AG (CH)	Location/Qualifiers				
FEATURES	1. 60				
source	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
BASE COUNT	15 a 12 c 17 g 7 t				
ORIGIN					
Query Match	0.8%; Score 22.2; DB 6; Length 51;				
Best Local Similarity	81.2%; Pred. No. 4.9e+05;				
Matches	26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
OY	1239 CACCAGAGGGCGACACTGGGAGAAAGCCTTA	1270			
Db	36 CATTGACGGTACTCAGCTGCGAGAGCCTTA	5			
RESULT 24					
AX382518/c	AX382518	60 bp	DNA	linear	PAT 18-MAR-2002
LOCUS	Sequence 48 from Patent WO0208286.				
DEFINITION	AX382518				
ACCESSION	AX382518				
VERSION	AX382518.1	GI:19577269			
KEYWORDS	synthetic construct.				
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Sera, T.				
TITLE	Zinc finger domain recognition code and uses thereof				
JOURNAL	Patent: WO 0208286-A 48 31-JAN-2002;				
SYNGENTA PARTICIPATIONS AG (CH)	Location/Qualifiers				
FEATURES	1. 60				
source	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="Partial zinc finger domain oligomer."				
BASE COUNT	15 a 11 c 19 g 15 t				
ORIGIN					
Query Match	0.8%; Score 22.4; DB 6; Length 60;				
Best Local Similarity	81.2%; Pred. No. 4.9e+05;				
Matches	26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
OY	1239 CACCAGAGGGCGACACTGGGAGAAAGCCTTA	1270			
Db	36 CATTGACGGTACTCAGCTGCGAGAGCCTTA	5			
RESULT 25					
AX163386/c	AX163386	51 bp	DNA	linear	PAT 22-JUN-2001
LOCUS	Sequence 6714 from Patent WO0140521.				</

Best Local Similarity 64.7%; Pred. No. 5.5e+05;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
OY 2475 CTTCCTGTTGGTCTTCCTCCGATGATCCACCTTCACCTATTT 2525
Db 51 CTTCCTGCGGGCGGTGGCTCCCTCCATTTCTTCACGATGACATATTT 1

RESULT 26
AX115765/c 51 bp DNA linear PAT 11-MAY-2001
LOCUS AX115765
DEFINITION Sequence 888 from Patent WO0129262.
ACCESSION AX115765
VERSION AX115765.1 GI:14032707
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Picoult-Newburg, L. and Pohl, M.
JOURNAL Patent: WO 0129262-A 888 26-APR-2001;
Ochid Biosciences, Inc. (US)
FEATURES
source
Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 11 a 9 c 14 g 17 t
ORIGIN

Query Match 0.8%; Score 21.8; DB 6; Length 51;
Best Local Similarity 70.7%; Pred. No. 7.3e+05;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1969 GCGAGTCACACCTCATTTAGACACGAGACACATTAGGA 2009
Db 42 GCGCTGTGACACCTCATTTAGACACGAGACATTACCAAGA 2

RESULT 27
AR036764/c 41 bp DNA linear PAT 29-SEP-1999
LOCUS AR036764
DEFINITION Sequence 6 from patent US 5800984.
ACCESSION AR036764
VERSION AR036764.1 GI:5954620
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Vary, C.P. H.
TITLE Nucleic acid sequence detection by triple helix formation at primer
JOURNAL site in amplification reactions
FEATURES Patent: US 5800984-A 6 01-SEP-1998;
source Location/Qualifiers
1..41
/organism="unknown"

BASE COUNT 6 a 16 c 7 g 12 t
ORIGIN

Query Match 0.8%; Score 21.6; DB 6; Length 41;
Best Local Similarity 75.0%; Pred. No. 8.2e+05;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 374 GCGAGGGGAGCGCCCTGAGAGAGAGAGAAAATG 409
Db 39 GCGTTCTGATCGCTTGAGAGAGAGAGAAAAG 4

RESULT 28
AF062523 60 bp DNA linear ROD 30-OCT-2001
LOCUS AF062523

DEFINITION Mus musculus antimicrobial mRNA sequence.
ACCESSION AF062523
VERSION AF062523.1 GI:16516872
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 60)
AUTHORS Ajidagba, P.A.
TITLE Direct Submission
JOURNAL Submitted (30-APR-1998) Veterinary Microbiology, Tuskegee
University, Carver Research Foundation Old Montgomery Road,
Tuskegee, AL 36088, USA
FEATURES
source Location/Qualifiers
1..60
/organism="Mus musculus"
/strain="C.D2 Vll-6"
/db_xref="taxon:10090"
/cell_type="macrophage"
/tissue_type="peritoneum"
/note="adherent peritoneal exudate cells; associated with
antimicrobial activity; similar to rearranged antigen
receptor"

BASE COUNT 21 a 11 c 19 g 9 t
ORIGIN

Query Match 0.8%; Score 21.6; DB 10; Length 60;
Best Local Similarity 63.5%; Pred. No. 8.6e+05;
Matches .33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 369 CTGAGGAGGAGGAGCGCCCTGAGAGAGAGAGAAAATGTCACCTGAGAC 420
Db 1 CTGAGGAGAACTGAGAGAGGTGTGTGCGCAATGAGAGAGTCGCCACTGAGAC 52

RESULT 29
AX159660/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX159660
DEFINITION Sequence 2988 from Patent WO0140521.
ACCESSION AX159660
VERSION AX159660.1 GI:14540991
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
FEATURES Patent: WO 0140521-A 2988 07-JUN-2001;
source Curagen Corporation (US)
Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc-feature
26
/note="2 of 2 allelic variants (2987 is other entry)
Accession number c942708452"

BASE COUNT 20 a 9 c 12 g 10 t
ORIGIN

Query Match 0.8%; Score 21.4; DB 6; Length 51;
Best Local Similarity 71.8%; Pred. No. 9.7e+05;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 2723 GAGAGCTGTCTTGTTCATATAAATCTTCTTACCC 2761
Db 43 GAGCTTCTTCTTGTTCATATAAATCTTCTTCAACC 5

RESULT 30

LOCUS	AX449255	60 bp	DNA	linear	PAT 03-JUL-2002
DEFINITION	Sequence 33 from Patent WO0206327.				
ACCESSION	AX449255				
VERSION	AX449255.1	GI:21698013			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Wang,Z. and Xiao,W.				
TITLE	A method for prognosing cancer and the proteins involved				
JOURNAL	Patent: WO 0206327-A 33 24-JAN-2002;				
	Northwestern University (US)				
FEATURES	Location/Qualifiers				
source	1..60				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="primer"				
BASE COUNT	11 a 16 c 16 g 17 t				
ORIGIN					
Query Match	0.8%; Score 21.4; DB 6;				
Best Local Similarity	66.0%; Pred. No. 9.9e+05;				
Matches	31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;				
OY	89 TCAGATCCGCGCGTGCACCCGCGTTCATCTGCTTCGAGACTT 135				
Db	6 TCTGATCCGAGGTGAGTACTGACTTACACACGCTCTCCGAGCTT 52				
RESULT 31					
LOCUS	AX158732	50 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 2060 from Patent WO0140521.				
ACCESSION	AX158732				
VERSION	AX158732.1	GI:14540063			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 50)				
AUTHORS	Shinkets,R.A. and Leach,M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and				
	methods of use thereof				
JOURNAL	Patent: WO 0140521-A 2060 07-JUN-2001;				
	Curagen Corporation (US).				
FEATURES	Location/Qualifiers				
source	1..50				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	25..26				
	/note="Nucleotide deleted between bases 25 and 26				
	Accession number cg38420254"				
BASE COUNT	15 a 14 c 12 g 9 t				
ORIGIN					
Query Match	0.8%; Score 21.2; DB 6;				
Best Local Similarity	69.0%; Pred. No. 1.1e+06;				
Matches	29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;				
OY	2278 AAGGAAATTCGTGCTCATTTTCAGAGCCCTGCCCTTCT 2319				
Db	8 AAGCAATATGCTGCGCAAAATATGAGAGGCTCTCACATTCT 49				
RESULT 32					
LOCUS	HSAD2S16	59 bp	DNA	linear	PRI 14-APR-1998
DEFINITION	Homo sapiens beta-adducin (ADD2) gene, exon 9, 5' partial sequence.				

[illegible]

REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0138586-A 539 31-MAY-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation 26
/note="single nucleotide polymorphism
Accession number cg41022625"
BASE COUNT 5 a 14 c 15 g 17 t
ORIGIN

Query Match 0.8%; Score 20.6; DB 6; Length 51;
Best Local Similarity 64.6%; Pred. No. 1.5e+06;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 133 CTTTGCCCTTCTCCAGAGACGACATGACGAGAAATGGCTA 180
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51 CTTTGCCCAAGACCAGCCCGACGACGAGAGAGATGACATGGCCA 4

RESULT 44
AX162153/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX162153
DEFINITION Sequence 5481 from Patent W00140521.
ACCESSION AX162153
VERSION AX162153.1 GI:14543484
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5481 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (5482 is other entry)
Accession number cg44002106"
BASE COUNT 12 a 14 c 14 g 11 t
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 1.7e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 475 TCTCCAGTCAGACGCTCTGACCAACATGTCGTGAGTCA 517
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51 TCTGAGGACGATATCTCTCACTCCCGGCTGTGCTCAGGCA 9

RESULT 45
AX162154/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX162154
DEFINITION Sequence 5482 from Patent W00140521.
ACCESSION AX162154
VERSION AX162154.1 GI:14543485
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)

AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5482 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (5481 is other entry)
Accession number cg44002106"
BASE COUNT 12 a 15 c 13 g 11 t
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 51;
Best Local Similarity 67.4%; Pred. No. 1.7e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 475 TCTCCAGTCAGACGCTCTGACCAACATGTCGTGAGTCA 517
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51 TCTGAGGACGATATCTCTCACTCCCGGCTGTGCTCAGGCA 9

RESULT 46
AR165679 52 bp DNA linear PAT 17-OCT-2001
LOCUS AR165679
DEFINITION Sequence 244 from patent US 6280932.
ACCESSION AR165679
VERSION AR165679.1 GI:16240661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Parma,D.H., Hicke,B., Bridonneau,P. and Gold,L.
TITLE High affinity nucleic acid ligands to lectins
JOURNAL Patent: US 6280932-A 244 28-AUG-2001;
Location/Qualifiers
source 1..52
/organism="unknown"
BASE COUNT 14 a 15 c 15 g 8 t
ORIGIN

Query Match 0.7%; Score 20.6; DB 6; Length 52;
Best Local Similarity 74.3%; Pred. No. 1.7e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 580 CAGAAGATCAGAAACACGACGAGATCCATTCCTGC 614
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 CAAGCGTCAGAAACAAATAGCTGATACATACCCG 38

RESULT 47
HUMNME1E 60 bp DNA linear PRI 15-APR-1994
LOCUS HUMNME1E/c
DEFINITION Homo sapiens (clones: ICRF c105H0563, ICRF c105E1086; subclone: BS23.13) nucleoside diphosphate kinase A chain (NMEL) gene fragment.
ACCESSION L05010
VERSION L05010.1 GI:472370
KEYWORDS nucleoside diphosphate kinase A chain.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 60)
AUTHORS Bafico,A., Valasco,L., De Benedetti,L., Calligo,M.A., Gismondi,V., Sciallero,S., Aste,H., Ferrara,G.B. and Bervillecqua,G.
TITLE Genomic PCR-SSCP analysis of the metastasis associated NM23-H1 (NMEL) gene: a study on colorectal cancer
JOURNAL Anticancer Res. 13 (6A), 2149-2154 (1993)
MEDLINE 94127836

PUBMED 8297127

FEATURES

source

Location/Qualifiers

1..60

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="17q22"

misc_feature 1..60

BASE COUNT 7 a 14 c 11 g 28 t

ORIGIN

Query Match 0.7%: Score 20.6; DB 9: Length 60;

Best Local Similarity 59.3%; Pred. No. 1.8e+06;

Matches 35; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1980 CTCATTAGACACACAGACACATTCAGAGAGAGCCCTTATTTTCAGAACTGTG 2033

Db 60 CTCACAGACAGAGAGATGTGTCAAGAGAGAAACATTCACAGCAGAAATGTGG 2

RESULT 48

AX158272/c

LOCUS AX158272

DEFINITION Sequence 1600 from Patent WO0140521.

ACCESSION AX158272

VERSION AX158272.1 GI:14539603

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 51)

AUTHORS Shimkets,R.A. and Leach,M.

TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: WO 0140521-A 1600 07-JUN-2001;

Curagen Corporation (US)

FEATURES

source

1..51

/organism="Homo sapiens"

/db_xref="taxon:9606"

misc_feature 26

/note="2 of 2 allelic variants (1599 is other entry)

Accession number cg3079374"

BASE COUNT 10 a 14 c 14 g 13 t

ORIGIN

Query Match 0.7%: Score 20.4; DB 6: Length 51;

Best Local Similarity 65.2%; Pred. No. 2e+06;

Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 752 CACAGTGTGATATAGTTCAGACCTGAACGAGGAGGAGATCTA 797

Db 48 CCCAGTGTGATATAGTTCAGACCTGAACGAGGAGGAGATCTA 3

RESULT 49

D50270/c

LOCUS D50270

DEFINITION Mouse Pig-f DNA, exon 3 5'-boundary sequence.

ACCESSION D50270

VERSION D50270.1 GI:1753184

KEYWORDS

SOURCE Pig-f.

Mus musculus DNA.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)

AUTHORS Ohishi,K., Kurimoto,Y., Inoue,N., Endo,Y., Takeda,J. and Kinoshita,T.

TITLE Cloning and characterization of the murine GPI anchor synthesis gene Pigf, a homologue of the human PI6F gene

JOURNAL Genomics 34 (3), 340-346 (1996)

MEDLINE 96374826

REFERENCE 2 (bases 1 to 52)

AUTHORS Ohishi,K.

TITLE Cloning and characterization of the GPI-anchor synthesis gene

JOURNAL Pig-f murine homologue to human PI6-F gene

REFERENCE 3 (bases 1 to 52)

AUTHORS Ohishi,K.

TITLE Direct Submission

JOURNAL Submitted (12-APR-1995) Kazuhito Ohishi, Research Institute for Microbial Diseases, Osaka University, Immunoregulation; 3-1 Yamada-oka, Suita, Osaka 565, Japan (tel:06-875-5233, fax:06-875-5233)

FEATURES

source

1..52

/organism="Mus musculus"

/db_xref="taxon:10090"

1..52

/gene="Pig-f"

<1..42

/gene="Pig-f"

/note="mouse Pig-f exon3 5'-boundary"

/number=2

43..52

/gene="Pig-f"

/number=3

BASE COUNT 11 a 11 c 10 g 20 t

ORIGIN

Query Match 0.7%: Score 20.4; DB 10: Length 52;

Best Local Similarity 65.2%; Pred. No. 2e+06;

Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1457 GCGTCACCTTACGTCGAATCAACCTCAAAACACACACAGAGACA 1502

Db 49 GCGTACCTTAAGAGAGAAATGAGATTCGAGAGCTCCAGAGATA 4

RESULT 50

AR040811/c

LOCUS AR040811

DEFINITION Sequence 40 from patent US 5811231.

ACCESSION AR040811

VERSION AR040811.1 GI:5961307

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)

AUTHORS Farr,S.B. and Todd,M.D.

TITLE Methods and kits for eukaryotic gene profiling

JOURNAL Patent: US 5811231-A 40 22-SEP-1998;

FEATURES

source

1..50

/organism="unknown"

BASE COUNT 15 a 16 c 8 g 11 t

ORIGIN

Query Match 0.7%: Score 20.2; DB 6: Length 50;

Best Local Similarity 68.3%; Pred. No. 2.3e+06;

Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2212 TCGACACATTCGTGTGATATGATGATGAGAGACTGTACTGG 2252

Db 48 TCGACACATTCGTGTGATGATGATGATGAGAGAGACTGTACTGG 8

Search completed: June 4, 2003, 09:16:59

Job time : 7203 secs